

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCA**ATG**GCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCACTATTACTTGTTCAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCACTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTGGTCAACTGGTCGCTGCCATCGTAGG
ATTTGTTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGTTGTGGTGCACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTTCCCTTGGAGTTGCTTGCTTCCAACCTGATTGGAATCTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAAGTATGAGATAGTG**TAA**CCCAATGTATCTGTGGCCTATTCCTCT
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAAACCTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTTGTATGTTCTAAGTCCACCTTCTATCCCATTCTATGTTAGATCG
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FIGURE 2

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><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
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NYEKALKQYNSTG DYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
```

Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGCGCCGCTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAAGTCAGT
 GCCACAGCCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCCTGGGGCGGGCGGACCGGACTGGG
 GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT
 GTTCCCTCTTTTCGGGGTCTCTACCAGAAGAGGTTCTTGGGGTTCGCCCTTCTGAGGAGGCT
 GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG
 GGAATAAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAATTC
 TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAAACTACCTAAATGATCGTCTTTG
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
 CACATAGCCCACTTCTTAGGGACTGGAGGTGCCGTACTACCATGGGTAATTCCTGTATCTG
 CCGAGATGACAGTGGAAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCTGTTTCGGCCACCAAGGAGGGGC
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTGGACACACT
 GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
 GAAAAGTGTCTGCCCCGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
 TGATAAGATTTGATGTTTTGCTTGCTGTCATCTACTTTGCTCTGGAATGTCTAAATGTTTC
 TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRKKQNV DGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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FIGURE 6

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107
<subunit 1 of 1, 231 aa, 1 stop
<NX(S/T): 0
MEEGGNLGGLIKMVHLLVLGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFYHGLSSLCNLGCVLSNGLCLAGLALAIRSL

```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AAATTAGATTTTAAGCCCATTTCTGCAGTGGAAATTTTCATGAAC TAGCAAGAGGACACCATCTT
CTTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGT
GCTAGGCCCTCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAG
ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAAACTTGGCAGCC
AGAACTTTTGATAAAAAGGGATTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTA CTGTGCTTCTGGATGTGACCGACCCAG
AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGT
CTGATCAATAATGCTGGTGTTCGCCGCTGTGGCTCCCACTGACTGGCTGACACTAGAGGA
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAAATGTCTCCAGTGTGGAGGTGCGCTTGCA
ATCGTTGGAGGGGCTATAC TCCAATATGCAGTGAAGGTTTCAATTGACAGCTTAAG
ACGGGACATGAAAGCTTTTGGTGTGCAGCTCTCATGCATTGAACCAGGATTGTTCAAAACAA
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAAC TCGCCATTGGGGAGCAGCTGTCTCCA
GACATCAAAACAATATGGAGAAGGTTACATTGAAAAAAGTCTAGACAAACTGAAAGGCCAA
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
GTCCTCTCCCTAAGACTCATTATGCCGCTGGAAAAAGATGCCAAAATTTCTGGA TACCTCTG
TCTCATATGCCAGCAGCTTTCGAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
TCCCAAGGCAGTGTCACTCAGCTAACCACAAATGTCTCTCCAGGCTATGAAATTGGCCGAT
TTCAAGAACACATCTCCTTTTCAACCCCATCTCTTATCTGCTCCAACCTGGACTCATTAGA
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCAGGGTCCCTG
CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCCTGT
ATTTAGGCTTTGGCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG
ATCTTTACCGTGGCCTGCCCATGCTTATGTGCTCCCAAGCATTTACAGTAACTTGTGAATGTT
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FIGURE 8

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><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
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LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

CGGGGCTGTTGACGGCGCTGCG**ATG**GGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCTTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGCGCTCGCCACCACT
 GTAGTCATGTATCCCAACCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCCGCGCTCGTGCTGGAGGAAATGGA
 AGCAACTGTCGAGATTGACAGCGGAATATGATTCTCTTCTCTTGCCTTTCTGCTTTTCTGT
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTTGGAAGCTCTGGCTTTACGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATTGTGGGTAAAAACAGCAAAATCCACCCGCTTACCAG
 CTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTCTGTCACAGAAGACACAA
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA
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 CACACCAGTGATCTGAACATATCGCCAGAAGGGCGTGATTGACGTCTTCTGTCATGCATGGA
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 GAGGAAGAATTTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTTGAAAAGGACG
 TGGACGTCAACCTGTTTGAAGCAGCATCCGCATCTGGGGGGGCTCCTGAGTGCTTACCAC
 CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC
 CTTTCAAGAACCATCTCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTACGTGGAGTTCGG
 GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTACGAGGCGAGTGGAGAAGGTGACACAGCA
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG
 GCCTCTTACCCACCTTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGAAGCAGGACACAGCTGCTGGAAGACTACGTGGA
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 GGGACGCTGGCTCTGGGCTCTACCACGGCTGCCGCCAGCCACATGGAGCTGGGCCAGGA
 GCTCATGGAGACTTGTATACAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
 TGCACTTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCCGGCTCACAGGGGA
 CCGCAAATACCAAGGACTGGGGCTGGGAGATCTGTCAGAGCTTTCAGCCGATTACACCGGGTCC
 CTCGGGTGCGTATTCTTCTCCATCAACAATGTCCAGGATCCTCAAGCCCGCAGCTAGGGAC
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA
 CCCAAACCTGCTCAGCCTGGACGCTTACGTGTTCAACACCGAAGCCCAACCTCTGCTTATCT
 GGACCCCTGCG**TAG**GGTGAGTGGCTGCTGCTGTGGGGACTTCGGGTGGGCAGAGGCACTTG
 CTGGGTCTGTGGCATTTCCTCAAGGGCCACGTAGCACCGGCAACCGGCAAGTGGCCAGGCT
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 GGCCCTCAGCTTGTGTTGATGCGGGGTGGGCTGGGCGCTGGAGCCTCCGCTGCTTCCCT
 CAGAAGACACCAATCATGACTACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCGGACCA
 GAGGGGGCTTCTGAGGTGTCCTTGGTACTGGGGTGACCGAGTGGAACCCAGGCTGCAGC
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 CTCGACAGGCTCAGGCTCCAGGGCTGGCTCTGGTGTTCACAGCTGGACTCAGGAGTCCCT
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FIGURE 10

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SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLCGLLFYINLADHWKALAFRLEEELQKMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGQTQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTLPSSRAEVP TKPPLPPARTQGTVPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFFESTIRILGGLSAYHLSGDSIFLRKAEDFGNRLMPAFRTPSKI
PYSVDVNIGTGVAHPPRWTS DSTVAEVT SIQLEFREL SRLTGDKKFQEA VEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQW IQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLTFFVGE LAHGRFSAKMDHLVCF LPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLREPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA
```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

SGGCGCCGCTAGGCCCGGGAGGCCGGGCCGGCCGGGCTGCGAGCGCTGCCCCATGCGCCGC
 CGCCTCTCCGACAGATGTTCCCTTCGCGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
 AGGTCGGGTTGCTCTCCGGCGGCCCTCCCTCGGAAGTGTTCCGTCTTCCACTGTTTCGTGGC
 CTGCCTCTCGCTGGGCTTCTTCTCCTACTCTTGCTGAGCTCAGCTGCTCTGGGGACGTGG
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 GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCTGTGCCCCACATGCGCCGCTTCTCTGA
 GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC
 CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCAGCGGATACATTGCCAT
 CACGACAGTTGACCTGCTCCTCTCTCAACAGGAGAGCTGGACTTGGCTTCTCTAGGCTGGGC
 CCTTCCAGCTGGGCTCCCGGAGCTCCACGCTCTCTACCTATACAAGACCTATGTCTGGCGGC
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 CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC
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 GGACCCCCCTGCCTTCTGTCTACCCCTACTCTGACCTCCTTACAGTGCCCAGGCCTGTGGG
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FIGURE 12

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><subunit 1 of 1, 327 aa, 1 stop
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GQGQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

CAATGTTTGCCTATCACCTCCCCAAGCCCTTTACCTATGCTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCCATCAGGGATTGGGCCTTCTTCCCCCTTCCTTCTGTGCTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCAGCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG
TGCGCCTATTAAAGTGGTGTGTTATGATTCTATACCTAATTTATACAAGAATATTAAAGC
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FIGURE 14

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PRGEGEKVGDG
```

Important features:**Signal peptide:**

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

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FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
 GAGCATGTCCGCGCCGGGGAAGGCCCGTCTCCGCGCCGCATAGGCTCCGGTCCGCGCTGG
 GCCCGCGCCGCTCTGTCCCGCCCGGCTCCGGGCGGCCGTAGGCAGTGCGCCGCGCG
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 GCGGCGCGCCGCGCGCGCTGCGCCGCGCTGCAAGCAGTGGCGGCCCGAGGGGCTGGC
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 GCCCCAGATACTCTGCCAACCGCACGGTCACCTGATTCTGAGTAACAATAAGATATCCG
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 GGCTAAACCTTTTCGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTTGATTATCTTGG
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 GAATTGCCGCTCTTCTACATGACTCCATCTCATCGCAAGTTGTTTGAAGGAGACAGCTT
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 ACTGGCTTCACGGGGATGACCTGTACCGTGTTCAGAAAAGTGGCAGCCTCTGATCGTACAGG
 ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGAACCTGGATAAGCAGCTGAGCTTTAAGT
 GCAATGTTTCAAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT
 AAGACTATTACAGTT**TAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAAATAACCTTATTA
 AAAGATTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAACCTA
 ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCCTTTGATTCCTTT
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 ATCAAAATTTTTGGCAGAAAAACAAATATGTCATATATCTTTTTTAAAAAAGTATTTCAT
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 TTGAATGAATGAACGAAAAAAAAAAAAAAAA

1007467.2301

FIGURE 16

MEPPGRRRRGRAQPPLLLPLSLLALLLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSLELAQVLPDPTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
 FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDDPPELPSFYMT
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGCCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLAGITA
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNL
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVMDIASNIMLA
 DERVLWLAQREAKACSRIVQCQLRIATYRLAGGAHVYSTYSPNIALEYVIKSTGFTGMTCT
 VFQKVAASDRDTGLSDYGRDPEGNLDKQLSFKCNVSNFTSSIALKVCYIILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
 384-390, 403-409, 554-560

FIGURE 17

GCGTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGTGGGCCTCTCGGTGCTGCTGACGGCGGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAATTCGGAAAAAGAAAACATTTCGTCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA
TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVKKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

1007407-121301

CTGTGCTCTTTGCTTAGCCGCAGTCGCCACTGGCTGCTGAGGTGCTCTTACAGCCTGTTCAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACCGCTGCCATGCCCAGTGACGGTAACCCGCACCACCATCACAAACCACCAGACGTCTATCTTCGGGCCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCCTGGGTCTCTTCGCTGCTGACGTGGTGTCTACCTGCGTGGCCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGACGGGGTCCATGGGCAACTGGTCCATGTTACACCTGGTGCTTCTGCTTCTCCGTGACCCCTGATCATCTCATCGTGGAGCTGTGCGGGGTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCCATCACCTTCGCCCTGCTATGCGGCCCTCTTCTGCCCTCTCGGCCCTCCATCATCTACCCACCACCTATGTCAGATCTCTCTGTCCACGGCCGTTCGCGGGACACGCCATCGCGCCACCTCTTCTCTCTGCTCATCGCTGTGTGGCTTACGCCATCGGAAGTGGCCTTGACCCGGGCGCGGCCCGCGGAGATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCTGTGCTGCATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGTGC GTGGCGGTGTACGCCATCTGCTTCATCTAGCGGCCATGCCATCCTGCTGAACCTGGGGGAGTGCACCAACGTGTACCCATCCCCCTCCCGAGCTTCTGTGCGGGCTGGCCTTGCTGTCTGTCTCTCTATGCCACCGCCCTTGTTCTCTGCGCCCTCTACCAGTTGCATGAGAAGTATGCGGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGACGCCATGCCTACTACGTGTGTGCCTGGGACCGCCGACTGGCTGTGGCCATCTTGACGGCCATCAACCTACTGGCGTATGTGGCTGACCTGGTGCACCTCTGCCACCTGGTTTTTGTCAAGGTCTAAGACTCTCCCAAGAGGCTCCCGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTTCCCGCCTTTCCCTCTGTTTTTCTCTTCTGCTCCCTCCCTCCCACTTTTCTTCTTCTTCCCAATCTCTTGCACTCTAACCAGTTCTTGAGTGCATCTTCTTCTTCTTCTTCTCTCTGCTGTCTTCTCTCTGTGTTTTTTGTTGTTGCCACATCTGTTTTACCCCTGAGTCTTCTCTCTTTCTCTTTTCTTTTTTTTTTTTTTTTTTTTTTATAGACGGATTCTCACTCTGTGGCTTCAGCTTTGAGTGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTTCAAGCGATTCTCTCCCGCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTTTCCACTCTTCTTTTTTCTCATCTCTTTTTCTGGGTTGCCTGTGCGCTTCTTATCTGCCTGTTTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCTGAGACTTCTTTCTCTCCTTGCCCTCCACCCCTCCAAGGTGCTGAGCTCACATCCACCCCCTTGACGCGCTCCATGCCACAGCCCCAAGGGGGCCCATTGCCAAAGCATGCCTGCCACCCTCGCTGTGCCTTAGTCAGTGTGTACGTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCTCCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCCCTTTAAATTAAAAACATATATATATATATATTGGAGGTCAATAATTCCAATGGGCGGGAGGCATTAAAGCACCAGCCCTGGGTCCCTAGGCCCGCTTGGCAGCTCAGCCCTTGCACAGAGATTGGCTCCAGAATTTTTGCCAGGCTTACAGAACACCCACTGCTTAGAGGCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTTCATCCCACTATTTCTGTGCTATGAAAAAG

FIGURE 20

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTTTTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLLIILIVELCGLQAREPLSWRNFPIITFACYAALFCLSASIIYPPTY
VQFLSHGRSRDHAIATFFSCIIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFKV

```

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

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AAGCTTGCCACCATGCCCTCTAAATTTCTGATTTTATGATAGACGCGGGTTTCCACATGTGGCCAGCGTGTGT
 TTGAAGCTGTGACCTCATGATCCCTCATCTCGGCTCCCAAGGTGGTGGATTACAGGATGAGCCATGAGCC
 CTGGCCAGCCTATGCATTTTAAAGAAATATCTGTATAGGCTCTGTCTCAATACATTGGGCCATACAGTGACCA
 AARACAGCTGAATTTCCCAAGACCAAAACAGCAGTGAGGAGAACCAAGAAACAGGAATTCARAAAGAGACA
 TTTATTCTACTACTATGACTAAGGTCACAAATGGSGTACCTTGCTGAGAGATGATTTTGAAGAGACTACAGGAG
 AGGACAGACTACCAAGAGSGGGGCCAGGAAGCTCTCTGACAGAGTGTGATTTTCAGCCCAAATGGAAAGATGA
 GARAGAGCTAGCCAGCCCTCAGAATGATCCAGAGAGATGGGGAGCACTACACTCACTACATCTTTGGCTGAGAA
 AATAGCATGGGATTGAGGAGGCTGGGGGAACACATCTTCGCGAGCTGGGCGAGGGAATTGAGGGCTTCGAGA
 AAGGCGAATGGCAGTAGCAGTAGAAGAAAGACAGGTTAGAGACAGGACCTTCGAGTGAGGAATCATTAGGCTAT
 ACACAGATATGGGCAAGCAAAAGCCGGGAGACATTTGATGGTAATGCTGAGGTTTGAGGCCAGCTAGATGGGACAG
 TGTGGTGATGTCAAAGGAAAGAGTGAGGAAGCAGGCGACAGCTGGGGAAGGTTGGGGGTTTTGGTTTCCA
 TCTTTCGCGAGTCTGCGGGAATGTGGATGGGAAGACAGAGAGGAGGACAGGGGACAGAGGGAAAGGAATCTTAA
 AGAAGTCTGATGAGGACACACT
 TCTCTGCTCTGCTCTCATCTCTCTCTGGGTGCTGGGAAGTGAGGAGTTAGCTGAAGTTTGGTCTCTCGGGGCTCT
 TCTGAATCTCATTTGTTCTGGGAGACATAATCACTCTCTCTAGCTTTCTTATCTATCTACATTTCCCTCTGAG
 CCATCGAGGCATATGTGGTGTCTCTCTCTAGCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 GGGGAAGGATCATGTGCTCTAGAGGGGACAGTACTTTTAATGGTTTACCCAAAGTGTAATGTGTGAGACATAGT
 CGGATGCTGCGCAAGTCCGGGCGGACCTTAACTCATCAGGAGATGCGTGCGCTGGCCAGGCTCCCTCCGTGAGTCT
 ATGACGCCCTCCGATGTTTCTGGCCACTTTGTCT
 CTGATGATCATCTGGGGTCTCCCTCTTTCT
 ACATGAGCTCTAACTATGCCACCTCTCCACCTCTCTGACCTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 TCCACCTCCCTCATCTCTCAGGATTTCTCCAGTGGTGAGGACAGGACAGCTGACCAAGCTCTGACAGCTCTGGCCAGG
 CGCGATGGCTCACTCATTTAGTGTGAAGGCTGTGAGCAAGCCAGTGACTCACTCTGCTGCTCTGGAATCCAGCT
 TTTCTCTCTATTACAGCTACAGCGAGGCGCAACAGAGGCTCTGCTTTGACAGGAGTGGCTGAGCAAGTTTGCA
 TCGCGAAGCCAGCTCCGAGCATGCTCTCTGGTGATGGCGAGGACTCCACTGATGACTCATATGATGAGGACT
 TCTGCTGGGGAAATGGACACAGCATGCTGCTGGGAGCTGCCCTGGGGCGCACTCTCCAGGACCTGTTCCAGCGCC
 ACGGTTCTCCGCGCTGTGGCCGAGGGCTCTGTGAGAGCTGAGAGCACTGCTCACAGACGCTGTCCCCAGATCA
 CCTGTGACTCTAGCTCTGACAGCTGAGAGATGGGTTGTGGGCTCCCCGCGGGCTGGCTCTCCAGCTCTGCGG
 GCTGTGACTGCTCTCTGCGCAAACTGCTCCCGCAGCGGAAAGTGCTCTCCGACAGCTGGGCGCTCTGAGCGCT
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 GGGTGGTGCTCTTAGATGAGGATAGGACAGAGCAGAGAGAGCAAGTGAAGCATATGCTCTGGCATTCTCTCT
 CTCCCGGCTCTGCTGACAGGCGACAGCCCTCTGTGCCCCAAGTGTGGGCTCAAGGCTCTCCAGCAGAGCTCAGAGCT
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 GCGTGGGGGCGCATGCTGCCGCCACTCTCCGGGCTCTGCGGGGGTGGCCGGGCGCTCTGGGCACTGGGCTACG
 GCTGTGGCAGACATGATGTCTCATGTTCTTAAATGCCACACACATTTCTCTCTGGATAATGTGAACATGAT
 AGGGGTGTGACGTGGGCTGTGAGGTTGGGTTGGGAGGGGCGGCAAGCCCCACCTCCCATGCTCTCTCT
 TCTTCTCTGCTTTTCTCTCACTCTCCGATCTATGTGACGTGTTGTATAGAATACCCCACTCTGAGGGGCTGCT
 CTTCTGCTCTCCGGAGCCTATGGGTTGAGCGTCCCTCAAGGGCCCTTGCCAGCTGGGCTCTGTGCTGTGCTCT
 ATTCACTCTCTCATCTCTCTCTAAATCTCTCTCTTTTCTTTAAAGACAGAAAGTTTGGTCTGTTTCTTTCACT
 GGATCTTCTCTCTCTCTGGGAGGCTTTGGAATGATGAAGACATGTACCTCTACCCCTTTTCTGGGCCCTCTAATGG
 GCGCTGGGCGCTTTCCCAACCCCTCTAGGATGTGCGGGCAGTGTGCTGGCGCTCTCAGACCGCGGGCTGCC
 ATTCAAGCAGAGCTCTCTAGCGGGAGGTGGAGAAAGAGTGCTCTGTGTGCCACAGACTGGGACTCATGTT
 CTCTTAGAGAGGCGCAAGAGGAGGACAGGGGTGCGGCGAGTGTGACAGTATGCTCTCTGACAGGCGAGAAAT
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 GAAGGCGCAAGGCTACAGTACAGGCGCCCGCCAGCCAGGTTGAATGCCAGCTGTGAGGCGTCTCGGAC
 ATCTCGCATTTCAAGGTTACAGAGTCTGATGTTTATGTTTGTGGGAAGGTTGGGTGGCTTTAGAATATAGGCG
 CTGTGAGGCTTTGCGAGGTAGAGAGGCCCCAGGATGAAGACAGAGACAGCGGCAAGCACTCATATATAGT
 GGCTCATAGGTGTTTATTTTGTCTATTATGAAGATTTGTTTATTAATTAATATAAAATCTTTGTAATCTC
 TAAAA

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSLAQVNLSPFSPKVMHDPNYCHPSTSLHLCS
 LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSELDGLLGSPARLASQLLGDE
 LLLAKLPSPRESAFRSLGLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
 QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
 285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTT
 GGCACCCCTCTGCTCAGTGCACATTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGA
 CAGATTCCTTTAGACAGGACAACGTGTATATTTCAGTTCCCTGATTGTAAATACCTCCTAAG
 CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
 TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG
 AAGCCTACA**ATGT**TTGGCCTTAGCCAAAATTCTGTTGATTTCACAGTTGTTTTATTCACTTCT
 ATCGGGGAGCCATGGAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT
 TTAAACAATGGAATAAAACCTATTTCTTTGGAAAGTGAAGCAAACTTAACTCAGATAAA
 GAAATATAACCACCTCAAATCTCAAGCGAGTCAATCCCTCCTTTGAATCTACCCAACA
 CAGCCACGGAATAACAGATTTCTCCAGTAACATCAGCAGAGCATTTCTTTGGCAGCTCTAA
 AACCACATCTACCATTTCACAAGCCCTCCCTTGATCCATAGCTTTGTTTTCTAAAGTGCCT
 TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
 TGCTCTGTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAAAACTCCTGATA
 ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
 ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
 TCAAGAAAAACAACCTCTACAGCCTACCTTAAATTCACCAATAATTCAAAACCTTTTCCAA
 ATACGTCCAGATCCCCAAAAAGAAAATAGAAAATACAGGAATAGTATTGCGGGCCATTTTAGGT
 GCTATTCTGGGTGTCTATTGCTTACTCTGTGGGTACTTGTGTGTGGAAGAAAGGAAAC
 GGATTCATTTCCCATCGCGACTTATGACGACAGAAAATGAACAGTTCTGCGATTAGACA
 ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTTAGCTACTACAATCCAACCTTTGAAT
 GATTGAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCATGGATGACATACC
 TCCACTTCGTACTTCTGTAT**TAGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA
 CATCTAGCCTTTTGACAAATTCATCTTTCAAAAGGTTACACAAAATTACTGTACGTGGAT
 TTTGTCAAGGAGAATCATAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
 CCAAGGTTTTCTTTCTACAATTTTGGCCATCTGAGGCATTTACTAAGTAGCCTTAATT
 TGTATTTTAGTAGTATTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT
 TCACCATACAGCCCTGCCTCATAACTAAATAATAAAAAATTATCCACCAAAAAATTTCTAAA
 ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
 TTTCTTAAATGAAAATGAAGGGTGC'TTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
 GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
 TAGTACGTTATAATTTCTAGATCAGCACACATGATCAGCCCACTGAGTTATGAAGCTGA
 CAATGACTGCATTCACGGGGCCATGGCAGGAAAGCTGACCCACCCAGGAAAGTAATAGCT
 TCTTTAAAGTCTTCAAGGTTTTGGGAATTTAACTTGCTCTTAATATATCTTAGGCTTCAA
 TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

FIGURE 24

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVLGYLLCGKRKTDTSFSHRRLYDDRNEPVLRLDNAPEPYDVSVFGNSSYYNPTLNSA
MPESEENARDGIPMDIPLRTSV
```

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTGTCAGTCTGCAGCCGAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
AGCCCGAAGATTCACT**ATGTG**GAAAAATGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
AGGCGCGCAAGAGCTGGAGGCCCTCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGTCTACTCT
CTTAGGCCTTTCATTATCTTTGGCAGGACTATTGTGTGGTGGAGCCTGCATTTACAAGTAC
TCATGCCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
AATTCCCTTCGTGGAGGAGAGCCTAACTTCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
GGATGACAACATTGCAATCATTGATGTGCTGTCCCCAGTTTCTCTGATAGTGACCCGTCAG
CAATTATTCATGACTTTGAAAAGGAATGACTGCTTACCTGGACTTGTGCTGGGGAACCTG
TATCTGATGCCCTCAACTACTCTATTGTTATGCCTCAAAAAATCTGGTAGAGCTCTTG
CAAACTGGCGAGTGGCAGATTCTATGCCCTCAAACTTATGTGGTTCGAGAAGACCTAGTTGCTG
TGGAGGAATTCGTGATGTATTAGTAACCTTGGCATTTTATTTTACCAACTTTGCAATTAACAGA
AAGTCTTCCGCCTTCGTCGCAGAGACCTCTTGCTGGGTTTCAACAAAGTGCCATTGATAA
ATGCTGGAAGATTAGACACTTCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
CATTAAAGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
AAAAAAAGGAAAAAAAAAAAAAACTACTAACCACCTGCAAGCTCTTGTCAAATTTTAGTTTAAT
TGGCATTGCTTGTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTTATAG
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GTGTGTTTTTTGTTGTTGTTGTTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATG
GTGGAGCAATTTTAAATTTGAAATATTTTAAATTTGTTTTTGAACTTTTTGTTAAATATA
TCAGATCTCAACATTGTTGGTTTCTTTTGTTTTTTCATTTTGTACAACCTTCTTGAATTTAGA
AATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAAT
TTCATGAGACAGTCATTTTAACTAATGACGTGATTCTTTCTCACTACTATCTGTATTGTGG
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CCCTATAATAAATTTTACTCTATACAAAAAATAAAAAAAAAA

FIGURE 26

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
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<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVTRQILTGKELRVATQKEGSSSGRCMLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPFSFSDSPAIIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIIFYQLCNRKSFRLRRRDLLGFNKRAIDKCKWIR
HFPNEFIVETKICQE

```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCAGAGCAGCCCCGGGCACCCAGCAGCGACTCTCT
 CTTCCAGCCCAGGTGCCCCCCACTCTCGCTCCATTGGGCGGGAGCACCAGTCTGTACGCC
 AAGAACTGGTCTGGGGCACC**ATG**GTTTCGGCGGCAGCCCCAGCCTCCTCATCTTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
 CGCCACCCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAACCTGGGG
 GGCCCATACCCCCCACC**AACT**TCCTGGATGGGATAGTGGACTTCTTCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA
 TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCTTCCCCAAGAAGAAGTAC
 GTGGACCAGAGTGACCGGGCGGGGGCCCCGGGCCCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG
 CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACAGGAAGTCCA
 GGGACATGGGGTCCCAGTGGAGACACCAGAGCGCAGGAGGAGCCGTGCTCAGGGGTCTTGT
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCCAG
 GAAGCCCAGGGACCACTGGGTCCCCCG**AAAG**CCCTGTGCTTGCAGCAGTGTCCACCCAG
 TGTCT**TAAC**AGTCTCTCCGGGTGCCAGCCCTGACTGTGGGCCCCCAAGTGGTCACCTCCCC
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCCTTGGCCTCCCTGTGG
 TGCCAATCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA
 GGAATCTTACCAAGTGCCATCATCTTCACTCAGCAGCCCCAAAGGGCTACATCCTACAGC
 ACAGCTCCCTGACAAAGTGAAGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCAAACTACTTTTTAAACA
 GCTACAGGGTAAATCCTGCAGCACCCACTCTGGAAATACTGCTCTTAATTTTCTGAAGG
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTAAATCCTC
 TCAAGCGCTCTCAAGCACCCCGGCC**TGGGG**TGAGTTTCTCATCCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGA**ACT**CTTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTTGAAGGGACCTCCACCTGGGGAACTCCGAGGGCTGGGGAAGGGTTTCTGACG
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 TGTCACACAATATTGTCGTCAGTCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCACATAAACTTTATTCCGGCCTGAAAAAAAAA
 AAAGA

FIGURE 28

```
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><MW: 29191, pI: 4.52, NX(S/T): 0
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SPTSMGPQPTTLGGPSPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGAGACCCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAG**ATG**
 AAGTTCCAGGGGGCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGG
 CCCCCTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCC
 TGGGAGACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAGAGGCCGGAGGGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG
 GCAGGTTCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG
 CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCAATTCGACACGGAGCA
 GATGCTGTCCGCGGCTCCTGGCAGGGGGTGCCTGGCCACAGTGGTGCTTGGGAAACTTCTGG
 AGGCCATGGCATCTTTGGCTCTCAAGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG
 GTCTGGGGACTCCGTGGGTCCACGGATACCCCGGAAACTCAGCAGGCAGCTTTGGAATGAAT
 CCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGAGGGCCACCAAACCTTGGGACCAACAC
 TCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAGTGAGAGCCAGCAACCAGAATGAAGGGT
 GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC
 TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACAATGGCAGCAGCAGTGG
 TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCTCTCTGGGGA
 TCCAGCACCGGCTCCTCTCCGGCAACCACGGTGGGAGCGGCGGAGGAATGGACATAAACCC
 CGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGAGCGGGGAATCTGGGATTAGGGCTTCA
 GAGGACAGGGAGTTTCCAGCAACATGAGGGAATAAGCAAGAGGGCAATCGCCTCCTTGGGA
 GGCTCTGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT
 TGGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTAACTTTGACACTTCT
 GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGA
 AGCTCTCGCATCCCG**TGAC**CTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACT
 CCCTCCTTAAACACCACCTCTCATCACTAATCTCAGCCCTTGCCCTTGAATAAACCTTA
 GCTGCCCCACAA
 AA

FIGURE 30

```
></usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGGLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPHSGAWETSGGHGIFGSGGGLGQGGQGNPGLGTPTWVHGYPGNSAGSFGM
NPQGAPWQGQGGNGPPNFGTNTQGAVALPGYGSVRASNQNEGCTNPPPSGSGGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSGSSSSSGSSSGSSSGGSSSGGSSSGSSGNSGGSRGDSGSESSW
SSSTGSSNGNHGSSGGGNGHKPGCEKPGNEARGSGESGIQGFRRGQGVSSNMREISKEGNRL
GSGSDNRYRGQSSWSGGGDVAGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRNP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGTCCCTCCGGTCTCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGGGGCTGCTCACCG
 TGCCCTGGCTGGTGGAGTTTCTCTCCCTTTCCTTGACCATGTTGTTCCCTGGAATATTACGGGACATCTTCA
 CTCTCCTGCTGCCTGACACCGGAGCTTGGTGTGTGCGCAGGAGAGTGAAGGGAAGATGTTCTTCTTCTGGAAGAGG
 TGCTGCTACTTGTCTGCTTGGGCTGGCTTTCCAGATTCCACAGTCCCTGAGGACTTGTCTTCTTCTGGAAGAGG
 GTCCCTCATATGCTTTGAGGTGGACACAGTAGCCGCCAGAGCATGCTTGGACAATGCGCTGTGTTGGACAGC
 AGCTGCTCTACACTGCTGCCCTTACATCGGAGAGCTCCGGAATCTGCTGCTTCTGTTGGGTGTCAGGCAGTAGTG
 GACGGAGTGGGGCTTATGAGGAAATCACCCCCACCTACACAGGCTGGGAGCCAGCTTCCGAGACA
 CGCAGGGGCTCGAGGCAGAGTGCCTCCAGGCTTTTCCACAAACAGCCGCCCTGCTTCTGCGCGGACCGTAGAGT
 TCGTGGCAGAAAGATTGGATCAAACATGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGTTGCGCCAGG
 CAGAGTCACTTCTCCAGAGCAGCTGCTGACACAGGAGAGGAAGGGGGAGACCCAGCCAGCTGTTGGAGATCT
 TGTGTTCCAGCTGTGCCCTCACGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG
 GGGCTGTGCGGGCGCTGCTCCAGAGGAGACCCGGCAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGG
 TTGCACACAGAGAAGCTGTGCTTGGCTGTGACCAACATACACAGCATGATCAGGAGGGAGGTGAAAGCAGCAG
 TGAGTGCACACTTCGAGCCAGGGTCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGCGCCCTGAC
 GTGCTCTCCTTGGCCGTGGGGCCACGGGACCTGACGAGGAGTCTCCCCAGAGCATCTGGAAACAGCTCCTAGGC
 CAGCTGGGCCAGAGCTGCGGTGCGGCCAGTCTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTGTCTGTG
 GAGTTAGCTTCCCTCCTGTTGCAATCAAATTCTATCTAGGGCCCCCGGCACAGTACAGGCTGGAGAGAGGG
 CAGGCTGAAGGCTTCTGCACATGCTGCTTCTTCTGTGGAAGGAAGACTTACAGGGGCGGTTCCGCTGCAGCTG
 CTGCTGAGGCCAAAGAATTGTGGGCTCTGCGCAGACACAGGCCAAGGGAGTGGGACTGCTGCTATTCTTGCTA
 CGGGAGCTGTTGGAAGGCTCTGATGGGACGGATGAGATAGAGGCCCTGCTGGGCGCTCCACAGGCCCCAG
 TGCCACGGGACTTGTGAAGATTAGCAACACTGTCTAATCTGTTCTAGCCAGGCCACTGCCAGAACCC
 CAGCTAAGAGCTGTGAGTTGGTGCAGCCAAACCGGGCCTGCTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC
 CTGCTTGGGCTTGCACCGGCTTGAACCCCGCTCACGAGGAGCCCAAGTGCCCAATGCAGACCTCTCAC
 TGGTTGGGTGTAGCTGGCTCTACAGTCAGACTTCTGCTCTAAGGGTGTCTGCTGCTGGCATCCACACCGCGA
 ATCCTAGAGSAGGAGAGTTGGCCTGATTGGGATTATGGCAGAAAGTCCAGAGATGCGAGTCTGTTGAGTAGAA
 GAGGTGGTGTGTTTATCTTGTGATACTAAATGAATGAGTGTGTGGGCTTGTCAACACAGAACTCAGGCT
 CATTTGCTATCCAGCATCTCTAAAACCTTGTAGTCTTGAATTCAIGACAGAGCAAAATGACTCTCTGTTAAC
 TTATGAAGAAAGTTAAACAGTGAATCTTGGGAGTCTACATTTCTTATCACCAGGAGCTGGACTGCCATCTCCCT
 ATAAATGCCATAACACAGGCCGGGTCTGGTGGCTCATGCCTGTAATCCCGCAGCTTGGAGGGCTGAGTCCCTT
 GACTGCCGTGAGGTGAGGAATTCAAGACCAAGCTGGCCCAACATGGCAAAACCCCATCTCTACTAAAAATAAAAAA
 TTATTAGCTGGGCATGGTGGTGTGCTGCTGTAATCCAGCTACTCAGGAGGATGAGGCAGAGAGACCTGCTTGAAC
 CTGGAGGTGGAGGTTGCAGTGAAGCCAGGCTGCACCACTGACTCCAGCTCTGGTGAACAGAGCGAGACTTCTAG
 AAAAGGCTTACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTCCCCCTGTACCTCTCAGCCCCG
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCATTTAGAGCTTTTTAGAATAAA
 CTGGTTTCTTTTAAAAAAGGGCGGCCGCCCTTT
 TTTTTTTTTTTTTTTTTTAAAAAGGGCTTTTATTAAATTTCCCCACAGATGGCTCTGCAATCTGCCACAGCTC
 TGGGGCGTGTCTGTAGGGAAGGCCCTGTTTCCCTGAGGCGGGGCTGGGCTGTCCATGGGTCCGCGGAGCTG
 GCGGTCTTGGCGCCCTGCGCTGTGTCTAGCTGCTTCTGCGGGCACAGAGCTGCGGGGCTCTGGGGGACCGGG
 AGCTAAGAGAGGCTCTGTGTCAGGGGTGGAGGCTGTCTCTTAACCGACACCTTGAGGTGCTCTGAGATGCTG
 GGTCCACTGAGTGCACGGGAGCAGCTGTGGCCGCTGCTCTTCTYTAGGCCAGCTCTGGGGAACTAGGCTG
 GGGCCCTCTTTTGCAAAAGCCAGAGTGGGGTGGTGTGGGGGACTACTGAGGGAATGGCTCTGAGGAGCTACGCTG
 GAAGAGGCGCGCGGTTGTGGCTGACGCGGCTCTCTCTGAGCGCTCTCTCTGAGCCTCAGTTTCCCTTCCGCTTA
 ATGAAGAATCATGCGCTCTCGGTGTCTCAGGCTATTAGGACTTGCCCTCAGGAAGTGGCTTGGACGAGCGTCACT
 GTTATTTTTCAAACTCTCTGCGAGCTTGGCTGGGCACTCATGGAATGGCCCATGTCTCCCTCTGCTGCGTGGAC
 GTCGCGCTCGGAGTGCAGCAGCAGAGGCGGGGCCAGACGTCGCGCTGGGGGTGAGGGAAGCGCCCGCGGAGGG
 CCTCACAGGAAGTTGGGCTCCCGCACCAACAGGACAGGCGGGCTCCGCGCGCGCGCGCACACGCTCCAGG
 GCGCGGTAGCAAAAGTGGAGTGCAGCTGGGCTGCTGCGCAGCAGGTAGCCCTTGATGTCAGTGGCGAGCGCG
 TCGTCCGCCAGCTGGAAGCAGCGCCCGTCCACAGCAGAACAGCGGTGCGCT

FIGURE 32

MCFLNLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
 CPYIGELRKLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP
 SLRRTVEFVAERIGSNCKVHKIKATLVADLVROAESLLQEQLVTQGEEGDPAQLLEILCSQL
 CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
 IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

FIGURE 34

MSSNKEQRSADVILFALITILLYSSNSANEVVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
 GNKTLPSRCHQCIVIVSSSSHLGLGPEIERAECTIRMNDAPTGTGSADVGNKTTYRVVAH
 SSVFVLRRLRPQEFVNRTPTVFIFWGPSPKMQKPGSLVRVIQRAGLVFPNMEAYAVSPGRM
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPRLQRMPIH
 YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPST

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTTCCTCATAGTTGGGCTCTTCTAAAGGAAAAACACTAAAATGAGGAAGTCAAGCGGACCGGGAGCGACGAGCTT
 GAGGGAAGCATCCCTAGCTGTTTGGCGCAGAGGGCGGAGGCTGAAGCCGAGTGGGCCGAGGTGTCTGAGGGCGCTGG
 CGCAAAAGTGAAGAAGTCTTCAGAAACAGCTTCTTGGAACCCATGACCATTGAAGTCTTTGTGCACATTTATACCGT
 CTCAGGCTAGCAGCTCGAAACTAGAAGAAGTGGAGTGTGGCCAGGAGCGGACATCTCTTTGTGTGACCCCTGGC
 GGCCATATGGGACGTTGGCTTCAGACACTTTGTGATACACATGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG
 AGSCCTGAGGTTCACACTGGCTTGCCCTCTCTAGCCACAGCAGGCTGTCTTGGCTGACTTGAACGAGATCCCTCAG
 GTCACCCGTCAGGCTGGCTTCACCGTCCAGAAAGCCCGGAGGACCTGTGATCTTGGGCTGCGTGGTGGAACTCCCA
 AGGATGAATGTAACTTGGCGCTCGAATGGAAGGAGCTGAATGGCTCGGATGATGCTTGGGTGTGCTCTCATCCAC
 CCGGGACCTCTCGTCATCTGCGCTTAACAACCACTCTGGGACGCTACCAAGTGTGTGGCCGGATGCTGCGTGG
 GGGGCTGGCCAGGCTGCCAGCACTGTGACACTAGCCAACTCCAGGACTCAAGTATAGATGTGCAGACAGCTG
 ATTGAAGTGGATGAGGGAACACAGCAGTCAATGCTGCCAATCTGCTGAGAGCCACCCCAAGGCCAGGTCCGG
 TACAGCGTCAAAAGAGGTGGCTGAGGCGCTCCAGAGGTAACTACCTGATCATGCCCTCAGGGAACTCCAGATT
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGCAGCTACAACCCAGTGACCCAGGAACTGAAAGCC
 TCCGGCTCCAGCGCAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACGCCCCAGAGGCC
 CAACTCATCTGTCACCAAGGCCAGGCTCTCATTTCTGGAGTGTGTGGCCAGTGGAACTCCACCCCCAGGGCT
 ATCTGGGCCAGGATGGTCCAGTGTCAACCGCTACACCAAGACGGCGCTTCTCTGAGCACTCTCTCATCGAC
 ACCACCCAGGAGGAGACTCAGGCACTACCGCTGCAATGGCCAGCAATGGGTTGGGAGCCCGGGGACGCGTCT
 ATCCCTCTACATCTCAGCTGTTTGAACCCCTGAGTGCACATGGACATCTCCAGCTGGTCAATCCCTCGGGGCT
 CAGAGTGCCACAGCTTACTGTGAGTGTGGTGGAAACCCCGCCCTCGCTGCTGTGGCTGAGGAATGCTGTGCC
 CTCTACTCCAGCGACGCTCTCCGCTCTCCCGAGGGCCCTCGCGCTGTCACAGTGGGGCTGAGGAAGCGAAGGC
 GTCTACAGTGCATGGCCAGAAAGAGGTTGGAGCGCCATCCGCTGATCTAGCTGGGACCTCCAGGCAACAGC
 ATAAACCCAAAGGCTGTGGCGAGTGTGAGCTGGCTACTGGCACACTCTCTGTATGAGCTCCAAACTCGCAAC
 CTTGAGCAGATGCTGAGGGGGCAACCGCGCTCCCGAGACCCCAAGCTCAGTGGGCGCTGCTTCCCGAAGTGT
 CCAGGAGAGAAGGGGACGGGGCTCCCGCCGAGGCTCCCATCATCTCAGCTCGCCCGCACTCTCGAGACAGAC
 TCTATGAATCGTGTGGCGGCTCGGCATGAGGCACTGGCCGGCGCAATCTCTACTATGTGGTGAACAC
 CGCAAGCAGGTCACAAAATCTCTGACGATTGGACCATCTCTGGCATTCCAGCAACACAGACCGGCTGACCTCT
 ACCAGACTTGAACCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAAGTGTGCTGGGAGAGGCGGACAGCC
 ATGGTCACCTTCCGAATCGACCGCGGCCCAACCCGAGATCATGGCCAGCAAGAGCAGCAGATCCAGAGAGAC
 GACCTTGGAGCCAGTCCCGACAGCAGCAGCCAGCCAGCACCGGCGGCTCTCCCGCCAGAGCTCCCGACAGG
 CCGACCATCTCCACCGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCGTGGGAATGTTGGGTTCCCAATC
 CAGTCTCTTCCGTGTGGAGTCAAGAAGCTTAAGAAGTGGGAGACTGATTTGGGACCTGAGCCACAGCCCATCCCA
 TCCGCGCTGTCCGTGAGATCAGGGCTAGAGAGAAGGCACTTCCTACAGTTTCCAGTCCGGGCTCTGAACATG
 CTGGGAGAGAGAGCCAGCGGCCCTCTCGGCCCTACGTGGTCTCGGGCTACACCGGTCCGCTGTACGAGAGG
 CCGCTGGCAGTCTTATATCACTTCAAGGATGCGGTCAATGAGACACCATCATGCTCAAGTGTATGTACATC
 CGACAGAATACAAACAAACCCCAATCCATGGCTTTTATATCTAATTCAAGCCACAGACAGTGAACATGATGT
 GCTTACAGAAAGGATATGTTGGAAAGGGGCAAGTACTGGCACTTCATCAGCCAGCTCGAGCCAGAGACTCTCTAC
 GACATTAAGATGCAGTGCTTCAATGAAGGAGGGGAGAGCAGTTCAGCAACGCTGATGATCTGTGAGACCAAGCT
 CGGAAGTCTTCTGGCGGCTGGTGCAGTGCACCCCAACTCTGGCCCAACACAGCCGCCCTCTCTGAAACC
 ATAGAGCGCCGCTGGGCACTGGGCGCATGTTGGCTCGCTCCAGCGACCTGCCATCTGATTGTGGGGTCTGCT
 CTGGGCTCGCTTCTCATCATCTGTCACCTTCTGCTTGTGGGAGCGCTGGCTTAAGCAAAAACAT
 ACAACAGACTGGGTTTTCTCGAAGTGCCCTTCCACCTCTCGCCGTATACATGTTGCCATTGGGAGGACTC
 CCAGGCCACAGGCGAGTGGACGACCTACCTCACTGAGTGGCATCACTGAGCGGCTGTGCTAATGGATCCCATG
 AATAGGGGCTGCCCTCGGCTGAGTGGCTACCCGGGCACTGAAGCCCGCAGCAGCTGCCCGAGGCGAGCTTCAG
 CAGCAGGTGACACACAGGAGCTCGTGAAGGACATCCATTTGGCAATGGATATGCCCCAGATCCCAAGCTCAG
 ACAGGGGCTCCAGCTTACCGCGCAGGAGGCTCTTCTTATACACTGCGGACGCTCTCACTCCAGCTGCT
 CTCGAGCCCTATCAGACTGTCGCAACGCCAGGAGCAGCTGCTGCTGTGGGCGGCTCAGGGGTGAGGAGAGCC
 CCGACAGTCTCTCTGGAAGCAGTGTGGACCTCCATTTCACTAGGCGCCAGTCTGCTGTGGGCTTGTG
 CCAATTGAAGAGTGCACAGTCTGACTCTCGCAAGTGAAGTGGAGGAGCTGGTGTCCCCAGCACCCCGTAGGG
 CGCTAGTGAAGACAGGAACCTGGATCGACTCTCCCGGGCCACTGTGCGTGTGCTTTTGAACACCACT
 CTCACATTTAGGCAGAAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAGAAAGAAA
 AGACACAGAGAAATTTGTTATTTTCTTATATAGCCATATTTATATATATTATGCACTTTGAATAAATGTGTA
 TATGTTTTTATATTTCTGGAGAGACATAAGGAGTCTACCCGTTGAGGTTGGAGAGGGAATTAAGAAGCTGCCA
 CCTAACAGGAGTCACCCAGGAAGACACCGCACAGGCTGGCGGGGACAGCTCTAAGTGGGCGCTCTGCAAGT
 GCGAGGCGAGGCTCAGGAGGCCACAGATAAGCTGGCAAGGAAGAGTCCCGGACATGGTTCATCAGGAGA
 TGGAGGACACGAAGGGGACAGGTATCACAGCTGGAGACACCCACAGATGGCTGGATCCGGTGTACGGGAA
 ACATTTCTCTAAGATGCCATGAGAACAGACCAAGATGTGACAGCATATGAGCATTAAGAAACCTTCCGAAT
 CANTAATCCGTCGACACATATCTCTGAAAAACAAACACTGTAACTTCAATATTAATGTTATGTTCTCCCTGTAAA

FIGURE 36

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQASTVQKPGGTIVILGCVVEPP
 RMNVTVRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNLYLIMPSGNLQ
 IVNASQDEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARI IY PPEAQT IIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCAENEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTTPPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGKGGAPAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYVVVKKRQVNTSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGASQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWI PRGNNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMIYIPASNNNT
 PIHGFYIYRPTSDSDNSDYKKDMVEGDKYWHISHLQPETSYDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVG TGAMVARSSDLPYLIVGVVLGSIVL
 IIVTFIPFCLWRAWKQKHTTDLGFPRALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMRGCPSSAAVGYPGMKPQHCPGELQQQSDTSSLLRQTHLNGYDPPQSHQITRGPK
 SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQEPPAAVGQSGVRRAPDSPVLEAVWDPPFHSG
 PPCCLGLVPVEEVDSPDSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCTGTCATGATCCGGACCCCATTTGTGGGCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCGCGCAAC**ATG**CAGCCCACGGGCCGCGAGGGTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGGAGACCACGCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC
 AGCCTCTTCCACAGCCGGGTGTCCCCAGCGCCTCACTACCCAGGCCTCACTACGCCAGG
 CACCCCCAAAACCCTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTACGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCCTACTCTGAACCTGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
 ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCACCAAGTTCAGACAC
 CACATGTACACCAAGCTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCTTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGCGAGTCATTGGATCTGAGTTCATCGGGATTGGTGAAATATGACGGGACT
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAGTGGAAAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCCTGGAGGTCTCAAATGCCT
 CCCCATACCTTGTTCCAGGCCTTGTTGGCTGCTGCCACCATCCCAACCTTCACCAGTGGCTC
 TGCT**TGA**CACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCTCACAAAGCCCCCTCTCCT
 AGTTCATTACAAAGCATATGCTGAGAATAACATGTTACACATGGAAAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYQQLSTSCH
SHLVFPQNGHQATHLEVTKQPTNRVPPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTTGGTGGCTGTGGTCCGGTGTGCTGGTGCCCCAGCTGAAGCCAACAA
 GAGTTCGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
 TTTACAACCAGAATGTATCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
 GTGCTTGCCATGACGTGGAGGCCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTCATCATTTGTCTATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
 ACATGGCCTTCTCTGATGCTGGTGGACCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC
 AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAG**ATGGGCTGG
 TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTCCCTCCTT
 CTCCTAACTTTAGAAATGTTGTAAGTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTGAGGCGGCCCTCAGGAGTGGATGCGATCTGTCTCTCTGCTCCACTCTTG
 CCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCCTTGAAGATAAAAGCTGGGTCTTCA
 GGAAGTCTAGTGTCTGGGAGGAAAGCATGGCCAGCATTGAGCATGTGTTCTTCTGCACTG
 GTTCTTATCACCACCTCCCTCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAAGGTGCACTGGA
 AGCTGGTGTTCGCTGTCCCTGTGCACCTCTCGCACTGGGGCATGGAGTGGCCATGCATACT
 CTGCTGCCGGTCCCCTACCTGCACCTTGAGGGGTCTGGGAGTCCCTCCTCTCCCCAGTGT
 CACAGTCACTGAGCCAGACGCTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCTGTACTTTGGGTGCTCTTGTCCCTGAAGTTCGTTGACAGTGCATGGA
 GAGAAAATTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTTG
 TTTTATTTCTCTCA

FIGURE 40

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSDIRCKICPPYRNISGHIYNQNVSQKDCNCLHVVEPM

PVPGHDEAYCLLCECRYEERSTTTIKVIIIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE

QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGGTCCCCGA
 ACCAGGAAGGGTTGAGGGAAACAATCTGCAAGCCCCCGGACCCAAAGTAGGGGGCCCGGTGTGGGGTCTCTCC
 TCCCTTTGCATTCCCACCCCTCCGGGCTTTCGCGTCTTCTCGGGACCCCTCGCGGGGAGATGCGCGCGTGTATG
 CGGAGCAGAGATTTCGCTGCTGCTGCTCTACTGGCGCGGTCGTGATGGTGGAGAGCTCACAGATCGGCAGT
 TCGCGGGGCCAACTCAACTCCATCAAGTCTCTCTGGGGGGGGAGACCCCTGGTCAGGCGGCCAATTCGATCTCGG
 GGCATGTACCAAGGACTGGCATTCGCGGGCAGTAGAAGGGGCAAAAGCTCTGGGCGAGGCTACCCCTTGTAGCAGT
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCTGGCCTGCATGGTCTGTCCGAGA
 AAAAAAGAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCATATATGGGCATCTGTATCCGAGTT
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCCAGCGTCATTAC
 TCAAAACCATGACTTGGGATGGCAGAACTAGGAAGACACACACTAAGATGTGCATATAAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTGTCTGTGCTCGTCATTCTCGAACCAAACTCGCAA
 CCAGTGTCCATCAGGGGGAAGTCTGTACCAAAACAAGCAAGAGGGTTCTCATGGCTGGAAATTTTCCAGCGT
 TGGCAGTGTGCGAAGGGCCCTGTCTTGCAAAAGTATGGAAGATGCCACCTACTCCTCCAAAGCCAGAGCTCCATGTG
 TGTGAGAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
 CATGGTGGAAATAAGGTTGAGATGCGAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAA
 AAGGGAGAAAGAAAACATGAACATGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTTCCATTATG
 CRACTTGTCTATGTAATAATGTACACATTTTGGGAAATGCTATTATTAAGAGAACAGGCACACAGTGGAAAT
 ACTGATGAGTAGCATGTGACTTTCCAAAGATTAGGTGTGCTGGAGGAGAGGTTTCTTTCAGATTGCTGATTGC
 TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAAATCTCCTAGAATAACTTGTTA
 TACAATAGGTTCTAAAAATAAAAATGCTAAACAGAAATGAAACATGGAGCATTGTTAATTTACAAACAGAAAAT
 TACCTTTTGATTGTGAACACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAGAAAAAAATCAGTCAATAT
 TTCCAAATTAATGCAAAATAATGGCCAGTTGTTAGGAGGGCCTTTAGGAAGCAAAATAATACAAACAAACAG
 CCACAAATACTCTTTTTTTCAAATTTTAGTTTTTACCTGTAATTAATAAGAACTGATACAGACAAAAACAGTCTCC
 TTCAGATTCTACGGAATGACAGTATCTCTCTTTATCTATGTGATTCTGCTGTGAATGCATTATATTTTCCA
 AACTATACCCATAAATTCAGTATGATAAATACTTACACAGACAGATTTTCCAGATGGCAAAAAAATTTAAA
 GATGCCAATATATGTGGGAAAGAGCTAACACAGACATCATTTTCTTAAGATTTGGCCATAAOCCTATATTTT
 GATAGAATTAGATTGGTAAATACATGTATTATACATACTCTGCTGGTAAGAGACTTAAGCTGGATCTGTACTG
 CACTGGAGTAGCAAGAAAATTTGGGAAAACCTTTTCTGTTCTGTCAGGTTTGGCAACACATAGATCATATCTGCTG
 AGGCACAAGTTGGCTGTTCACTTTTGAACACAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT
 CATATAATTTTACTATGCAAGATGAATCAGTGTGAGGTCCTGCTCCGTACTATCCCTCAAAATATTATTATTATAG
 TGTGAGATCTCAAAATATCTCAATTCAGGAGGTTTCCAAAAATGCTACTCTGAATGAGACAGAGTAGTGAGG
 TTTTCAITCCCTCTATAAGCTTCTGACTAGCCAAATGGCATCATCAATTTTCTTCCAAACCTCTGCAGCATCTG
 CTTTATTGCCAAAGGGCTAGTTTCGGTTTCTGCGAGCCATTCGCGTTAAAAAACTATAAGTAGAATCTGTAAA
 AACTGCAATATGCTAATCTATAGACACACAGTTTCTAAATCTTTTGAACACCTTTACTACTTTTTTAAACTTT
 AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACATAAAGGTTATCTTATAGTCGTGACTTTAAACTTTTG
 TAGACCACAATTCACTTTTTGTGTTTTTCTTTTACTTAATCCCATCTGCAGTCTCAAAATTAAGTCTCCAGTAG
 AGATTGAGTTTGAGCCTGTATATCTATTAATAATTTCAACTCTCCACATATATTACTAAGATGATTAGACTTA
 CACTTTTCTGCAGAGGCTCGCAAAACAAAAAATTAATACTAGTCCATCCAGAACCAAAAGTTGTATAAACAGST
 TGTCTAATAGCTTGTGAATGAAATGGAACATTTCAATCAAACTTTTCCATATAACAAATTTATATATTTACAAT
 TTGGTTTCTGCAATATTTTTCTTATGTCACCCCTTTTAAAAATTTATTTTGAAGTAAATTTATTACAGGAAATG
 TTAATGAGATGATTTTCTTATAGAGATTTTCTTACAGAAAGCTTTGTAGCAGAATATATTGAGCTATTGAC
 TTTGTAAATTTAGAAAAATGTATAAAGATAAATCTATTAAATTTTCTCCTCTAAAAACTGAAAAAATAAA
 AAAAAAAAAAAAAAAAAA

FIGURE 42

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRC
NN
GICIPVTESILTPHIPALDGTNRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

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FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAA
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGCCAACATCAGTTTAAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACCTCTTATGTGAGAATGAGGAAGGA
 TAGCTGCATTTATTTAGTCAGTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAAATACTG
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA
 TCACCAGCTCCAGATTTTGGACCAAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCTACAACCTACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
 CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTGTCTCCTCT
 CCTGGTTTGGAGTCCTTCTCTCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC
 CTCACATGTGAACAAGCTTTTGCAGCTTCCCAGCAGCACCATTGAAAATATCTCTGTGTCTG
 TCCACCAGCCACAGCCCAACACATCAAACCTTGCTAAGCGGCGGATACCCCGAGTTCTAAG
 ATCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAATGTGCAGTT
 TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTGAAATTTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCCATCAGCTTGTATTGGAAGTCTTTAAGTGAGCCTTTGAATACA
 TCTTTATCAATGACCAGTGCAAGTACAGAACTCCACATATACAACCTCCGTCATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAACAGAGGAAGAGGATAGCTCACGTGA
 TGTGGAACACACAGTTGGTCAATGGCTCATTTCGTTAAAGCAGCCCTTTTGCTTTTTTGT
 TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCATAATCCAGTGCTTTGGGGGGCC
 AAGGCAGGCAGATTGCCAAGCTCAGGAGTTTGAGACCACCTGGGCAACATGGTGAAACTC
 TGCTCTACTATAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGTGCCTGTAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTSDWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFSPQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCGCGCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGGCGACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCGGG
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTGGGCGAGCGCCGCGCCTA
 CGGGCCCCCTTTTCTGCGCGACCGCTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCGGAACCCACGC
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCACAG
 ACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTCATCGTCCCCGAGAGCCGAGCCAC
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC
 TGTCTCCTGGCGCCCCGAGGCGCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTGCTGTGGCTGCAAGGGACCATGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT
 GCAAA**TAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCCCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCGGCCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAACC
 AAAATCCCACTGATGCCCATCATGCCCTCAGACCCCTTCTGGGCTCTGCCCGCTGGGGGCCCTG
 AAGACATTCTGGAGGACATCCCATCAGAACTGGCAGCCCCAAAATGGGGTCAGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCATCCCTACCCTAGCCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT
 GCATCTGTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA
 AAAAA

FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPFAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWD RQPPGVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEP PPRGSPNGSSSHSGAPGDP TPLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDL DKGFRKENCK

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGCGCGCGTGGCGCAGCGGCGACATGCGCGTTGTCTCAGAGGACGACTTT
 CAGCACAGTTCAAACCTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCTTGGCTGCAGAGGCCCGAGGACCGCTTCT
 GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTTCTTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCCAGCCACCGGGGA
 GGACCCGTGAGGGCTCAGACATCCTGAACCTACTTTGAGAGTACCTTGCCGTTGCCCTCCACCG
 TGCCCTCCATGCTGTGCTGGTGGCAACTTCTGCTTGTCAACAGGGTTGCAGTCCACATC
 CGTGCTCTGGCCTCACTGACGGTCATCTGGCCATCTTCATGGTGATAACTGCACCTGGTGAA
 GGTGGACACTTCCTCTGGACCCGTGGTTTTTTTTGCGGTCACCATTGTCTGCATGGTGATCC
 TCAGCGGTGCCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCTCTATG
 AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
 CCACCATCTTCTCTGCTCTGCATGGGACTCTACCTGCTGCTGCCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCTGTCTTGGCGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCA
 GGACTCCCTCAGTGCCCTTCCGGTGGCCTCCAGATTGATGATCCACACACCCCTCTCC
 GCCCATCTCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGCTCTTCTTCATACCC
 AGCCTCATCTACCCCGCGCTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
 GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCTGTACAACTTTGCTGACCTAT
 GTGGCCGCGCAGCTCACCGCCTGGATCCAGGTGCCAGGGGCCAACAGCAAGGCCTCCAGGG
 TTCGTGCTCCTCCGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACACAGCCCCGGGT
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCTGTG
 GGCTCAGCAACGGCTACCTCAGACCCCTGGCCCTCCTCTACGGCCCTAAGATTGTGCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTATGTGTGCTTGGGCTTAACACTGGG
 CTCAGCCTGCTCTACCCTCCTGGTGCACCTCATCTAGAAAGGAGGACACAAGGACATTTGGTG
 CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA
 GTGAGCCAGCTCCATGCCATTCCTGCAAGGCAGATATCCAGTCAATTAACAGAACT
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTACAGCTGATGGTTA
 ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTCGCCCTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAAGTGCAGCTCATCCAGCT
 GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCCTGAAGGGGTCTCCCTGGAATGGA
 AGTCCCTTGGCATGGTCAGTCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
 GCGGGTGAAACAACCTGCCACTAACCCAGACTGGAAAACCCAGAAAGATGGGCTTCCATGAAT
 GCTTCATTCCAGAGGGACGAGGGCCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
 TTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCTCAGATGAGTCAAGTGGGTG
 TTTCACTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCTAATAAATACTTGC
 GTATTCAAAA

FIGURE 48

MAVVSDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPGLQRPEDRFCGTYYIIFSLGI
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
 LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
 YGMTGSFFMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
 LLLSRLEYARYYMRPVLAHVFSGEEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLGF
 CVTYVFFITS LIYPVCTNIESLNKSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
 GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKT VVFQSDVYPALLSSLLGLSNGYLSTLAL
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
 305-330, 448-472

FIGURE 50

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLS DAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPKEKLYALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDL LPRALLSSL SGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL
KVLKADVLLTASGPAVKRITFS PPLPRHMQEALRRLHYVPATKVFLSFRFPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLLAS YTWSDAAAAFAGLSREEALRLALDDVAALHGFPVVRQL
WDGTGVVKKWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHG VASSPSHDLAKEEGSHPPVQQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT
 GGCAGCCTCTGAAAGCCACCCCTGTCCTGGAGGAACACGAGCGAGGGGAAGAAGCAGGAGACTCGTGTGGCAGGAA
 GAACCTCAGAGCCGGGAAGCCCCATTCACTAGAAGCACTGAGAGATCGCGGCCCTCCGACGGGTCTGAATTTTCCT
 GCTGCTGTTTACAAAAGATGCTTTTATCTTTAACTTTTGTTCCTCCCACTCTCCGACCCCGGGCTTGATCTGCAT
 CTTGACATTTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCAGCGGAAGGGGTTTCCAGAAGAACAAAGACCTTAAACAAGTTGCTG
 CTTCTCAGATGCCAAGACTATGATGAGGTTTCCAAAGAGGACTCGTGTGCTGAGAATGGGCCCTGTTGGG
 ATATAGAAAACCAACAGCCCTACAGATGGCTATCTTACAACAGGTTCTGATAGAGCAGAGTACCTGGGTTC
 CTGCTCTTGTGATAAAGGTTATAAATCATCACAGACCACTTTGTCGGCATCTTTGCTCAGAATAGGCCAGAGTG
 GATCATCTCCGAATTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACAGAAAGC
 CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACCCCAAAAGGCAATTGGTGTGAT
 AGGGAATGTAGAGAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCTTATGGACCCCTTTGATGATGACCTGAA
 GCAAGAGGGGAGAGAAGTGAATTGAGATCTTATCCCTATATGCTGAGAACCTAGGCCAAAGACACTTCAG
 AAAACCTGTGCCCTCTAGCCAGAAAGCCTGAGCGTCATCTGCTTACACAGTGGGACCACAGGTGACCCCAAAGG
 AGCCATGATAACCCATCAAAATATTGTTCAAATGCTGCTGCCCTTCTCAAATGTTGGAGCATGCTTTATGAGCC
 CACTCTGATGATGTGGCCATATCTTACCTCCCTGCTGCTCATATGTTTGAAGGATTGTACAGGCTGTTTGTGTA
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATGTGTTTCCCGCGGTGCCCTGACTCCTTAACAGGATTCACGATAAGGTACAAAATGAGGCCAAGACACCCCT
 GAAGAAGTTCTTGTGAAAGTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCAATGATAG
 TTTCTGGGACAAGCTCATCTTCTGAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCGTGTAATTTGCATCTGGAGC
 TGCCCCCATCTGCACTTCACTGACATGACATTTCTCCGGGACGAATGGGATGTCAGGTGTATGAAGCTTATGGTCA
 AACAGACATCAGAGTGGCTGTACATTTACATTTACCTGGGCACTGGACATCAGGTGTGTTGGGGTGGCCCTGGC
 TTGCAATTAAGCTGAACCTGGAAGATGTGGCTGACATGAACACTTTACAGTGAATAAATGAAGGAGAGGCTGCAAT
 CAAGGTCACAAAGCTGTTCAAAGATACCTGAAGGACCCGAGAAGACAGGAAGCCCTGGACATGATGGCTGT
 CAGTTACACAGGAGACATTTGTCGCTGGCTCCGGAATGGAACCTTGAAGATCATCGACCCTAAAAGAAGATTTT
 CAAGCTGGCCCAAGAGATACATTGCACCAGAGAAGATAGAAAATATCTACACAGGAGTCAACACAGTTGTTCA
 AATTTTGTACACGGGGAGAGCTTACGGTCATCTTAGTAGGAGTGGTGGTTCCTGACACCAATGTACTTTCCCTC
 ATTTGTCAGCCAGAGTGGGGTGAAGGGCTCCTTTGAGGAAGTGGCCAAAACCAAGTTGTAAAGGAAGCCATTTT
 AGAAGACTTGACAAAATTTGGGAAGAAAGTGGCCCTAAACCTTTTGAACAGGTCAAGGCCATTTTCTTCTATCC
 AGAGCCATTTTCATTGAAAATGGGCTCTTGACACCAACATTGAAGCAAGAGGAGAGCTTTCCAAATACTT
 TCGGCCCAAAATTGACAGCCTGTATGAGCACATCCAGGATAGAGATAAGGTACTTAAGTACCTGCGGCCCACTG
 TGCACTGCTGTGAGAAAAATGGATTAAAAACTATTCTTACATTTGTTTTCGCTTTCCCTCCTATTTTTAAAC
 TGTAAACTCTAAAGCCATAGCTTTTGTTTTATATGAGACATATAATGTGTAACCTTAGTCCCAATTAATCA
 ATCTGTCTTTCCCATCTTCGATTTGCTAATATTAAGGCTTCAGGGCTACTTTATACACATGCTGTGCTTCAA
 GATCCCAGTTTATGTTCTGTGCTTCTCATGATTCCAAACCTTAATACTATTAGTAACCAAGGTTCAAGGGT
 CAAAGGACCCCTGTGCTCTCTCTTTGTTTGTATAAACATAACTTGCCAAACAGTCTCATGCTTATTTTACA
 TCTTCTACTGTTCAAACCTAAGAGATTTTAAATCTGAAAAACTGCTTACAATTCATGTTTCTAGCCACTCCAC
 AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGCTCCGATGCTCTT
 CTGCGTAAATTAATTTGTGACTGAAGGGAAAGTTTGATCATACCAACATTTCTTAACTCTCTAGTTAGATA
 TCTGATCTGGGAGTATTAATAATTTGGGTCTATGACATCTGTCCAAAAGGAATGCTGTCTTAAAGCATTTT
 CAGTAGGAATCTGGGGAGTAAATCTGTTCCCTACAGTTTGTCTGCTGAGCTGGGAAGCTGTGGGGGAAGGAGTTGACA
 AGGTGGCCAGTGAATCTTTCCAGTAAATGAAGCAAGCACTGAATAAAACCTCTGAACTGGGAACAAAGATCT
 ACAGGCAGCAGAGATGCCACACACAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCCACCCTTGGATT
 AGAGTTCTGCTCTACTCTTACCACAGATAACACATGTTCTTCTGATAAATGTAAAGTCTTTAAAATAAAC
 TATTACAGATAAAAAA

FIGURE 52

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLLLFTKMLFIFN
FLFSPLPTPALICILTFGAAIFLWLI TRPQPVLPLLDLNNQSVGIEGGARKGV SQKNNDLTS
CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKG YKSS
PDQFVGIFAQNRPEWIISELACYTYSMAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLVKVIILMDPDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNI VSNAAFLKCV E HAYEPTPDDVAISYLPLAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFFAVPRLNRIYDKVQNEAKT PLKKFLLKLA
VSSKFKE LQKGIIRHDSFWDKLIFAKIQDSLGGVRVRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLP GDWTSGHVGVP LACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRKNI FKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSSLGVVVPD TDVLP SFAAKLG VKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPF SIENGLLTPTL KAKRGELSKYFRTQIDSLYEHIQD

```

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGCCGCGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG
 CCCGGGGCCCCTAAGCCATTCTGTAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT
 CCGGT**ATG**GACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAGCGG
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
 GACAGGGGCCGTGCTTTTCTGCTGGTGACTGTCTTGTCAATATCAAGTTGATCCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCATGAAGACCCAGAGCCAGCAAGACTATGATGAGGCC
 CTAGGCCGCTTGAGCCCCCAGCGCGCAGAGGCACTGGTCCCCGGCGGGTCTTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG
 AGGCCGGGAGCAGGGCCGGGCCATCCATGTCTTCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAACGCTGTGTTGACACGTACTACCTCATGAGGATGAGGCCATGGTGCTATTCTT
 CAACATGGTAGCGCCCGCCGAGTGCTCATCTGCATGTCAAGGATGAGGGCTCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC
 TGGAGGGACACATGGGCCTTCGTGGGACGAAAAGGAGGTCTGTCTTTCGGGGAGAAACATT
 TAAAGTCACCTGCCCTCTCTTCTGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCG
 TTCTGCAGCAAGTGTAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCAGACAAACAGGTCTCTAAGTGCTGTGCTGTCTATTGACAG
 GGAACCGACCCAAATTAAGTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCACAGGGGGTGCT
 CCTCAGATGATCAACAGTTTTTCATTGACGGCTACTATGAGGACCCATGGATGTGTGGCAT
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGATGCCCGCGTGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTCCGGAGGCCAAGTTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTCAGTTTCTGAGCCAAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCTGGAATGACCAGGGGTATGAACACA
 CGGCTGAGGACCGACACTACTGTACCGTGTGGAGACCATGCCCTAGCGTGGGCTGGGTGCTC
 AGGAGGTCTTGTACAGGAGGAGCTTGAGCCCAAGTGGCCCTACCCGGAAGAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCGTAACAACGCCGGGGCCGAGAGTGATCATCTCCTGAGC
 TTTCCCGATCCTACCCTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTTACGAGGCC
 TACTTCAAGAAGCACAAAGTTCAACACGGTTCAGGTGTCCAGCTCAGGAATGTGGACAGTCT
 GAAGAAGAAGCTTATGAAGTGAAGTTCACAGGCTGCTCAGTGAGGTGAGGTTCTGGACC
 ACAGCAAGAACCCTTGTGAAGACTCTTTCTGCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTTATCGAATGGAGAAAGATGATGACTTACCACCTGGACCCAGCTTGCCAAAGTGCCCTCA
 TATCTGGGACCTGGATGTGCTGGCAACCATCGGGGCTGTGGAGATTGTTTCGGAAGAGA
 ACCACTTCTGGTGGTGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC
 ACCCAATTTTCTGGAGCCACCCCCAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC
ATGAGACCTCTCTCAGGACCTGCGGGGCTGGGTACTGTGTACCCCGAGGCTGGCTAGCCCT
 TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGCTGGGGCTACCTTGTGTTTTAACA
 TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCTGCTCCAACACCCCGTTCTCGAGTT
 AAAAGTCTATTATTACTTTTACTCTTGTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG
 ATCCTTAGCAGCTCATCCTGCCCTTTGAATACCTCACTTTCAGGCCGTGGCTCAGAATTCTA
 ACCTATTATTAGACTGCTCTGAGGGCCTTGAAACAGGCCGCAAGCTTGAGGGCCTGGATTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAAACTGCTGTGCC
 CAACCCATGGACAGGCCACGTGGGGCCACATGCTGACACAGCTCACTCAGAGACCCCTTA
 CAGCTGACACAGGCCCTCCTCTCAGCCTTCTCTTGTCCAGATTTCGAAGCTGGATAAGTT
 GGTCAATTGATTAAGAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
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REQGRGIHVIVLNQATGHVMAKRVFDITYSPHEDEAMVLFNLNMPVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTHAFVGRKGGPVFGEKHSKSPALSSWGDVPLLKTDVPLSS
AEEAECHWADTELNRRRRFRFCCKVEGYGSVCCKDPTPIEFSPDPLDNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEPMDDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRSLYKEELEPKWPTPEKLWDWDMWMMRMEQRRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKEAYEVEVHRLLEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLDVGRGNHRLWLRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPEKEGAPGAPEQT
```

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAGGCCACTCTCTTGGAAACCACCACAC
 CTGTTTTAAAGAACCTTAAGCACCATTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA
 AAGGAGGGGAGATGGATGATTTCATCTCCATTAGCCTGCTGTCTCTGGGTATGTTGGTGGGATGTTA
 CGTGGCCGAATCATTCCCTTGGCTGTAAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGG
 GTGCTGGCTTCTCTGTGGAACCTGCTCTGGCAGTCACTGCTGAGGAGTACATGCCCTTTATGAA
 GATATTTCTTGGGGAAAACACCACCAAGCAAGTGAACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCCATGAACATGAGCAGAGCCACGACCACACAGACTGCATGCCCTATATTGGTG
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGGTAACTCCCATGTGCATTCT
 ACTGACGATCCAGAAGCAGCAGGCTCTAGCAATTCAAAATCACCACCAGCTGGGTCTGGTTGTGCCA
 TGCTGCAGCTGATGGTGTTCCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTCCCTTCTGATGCATGCT
 GGCCTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTTCTCGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGGCGGA
 ATAGGCGACAGCCACAAGCCGATGCCACGGGAGGAGAGGCCCTCAGCCCGCTGGAAGTGGCAGCCCT
 GGTTCCTGGGTCTGCTCATCCCTCTCATCTGTCACTAGGACACCAGCATTAAGTGTTCAGGTCCAGC
 CTTGGTCCAGGGCCGTTTTCCCATCCAGTGAGAACAGCCGCGCAGTGCAGCTACTCACTTCCCTCAGTC
 TCTTGTCTCACCTTGGCATCTCTACATGTATTCTAGAGTCCAGAGGGGAGGTGAGGTTAAACCTG
 AGTAATGGAAAAGCTTTTAGAGTAGAAAACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTT
 TATCTTTTAAAGGCCCTTGACATTTGCGTTTTAATATTTCTCTAACCCCTATTCTCAGGGAAGATG
 GAATTTAGTTTTAAGGAAAAGAGGAGAACTTCATACTCACAAATGAAATAGTGATTATGAAAATACAGT
 GTTCTGTAATTAAGCTATGTCTCTTTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTT
 AACATGGTTCCCAACATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGTGGAAGGTGATA
 GCACCCACTCACTTAGCTGAAGAGTGATCTAGTTAATCTGGATAGGCTCAGGAAATAGTAGC
 AAGACACATTGAAGCTCTCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT
 TAAACAGCTCCCTTGGCAGCTGCCCTCTCTGAATCCAGCCCTGCCATTCCATCAAATGGAGCAGGAGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCCTTGTCAAGTTCCTCTTGCAGAA
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 CAGTCAGATCACAAAGTGCTTTTGGAAATTAAGGGATATTAATTTTAAAGTGATTTTGGATGGTTAT
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 TTTTTTTTTAATTAATTTCTCTTAGCAGATCAGCAATCCCTCTAGGAGCCTAAATACTAGTCACTTTT
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 TTGATTTAAAGCTTATGGAATCATGTCTCTTGTCTCTTCGTCTTTCTTTGCTTTTCTTCTAACCCTT
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 CTTATCAGGACAACCACTCTCGAACTGTAATAATGAAGATAATAATATCTTTATCTTTATCCCCCTT
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 ATTTTTTTTTTCAATTTGCCAAAATTTTTGTAAACCCGTGCTTGTCAAATAAGTGATAATATGTAT
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 GGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCACTTGGCAACAATTGACATA
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 GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCCTTCAAACATATATGGTTGCCTAGATTCTCTCTGGA
 AACTGACTTTGTCAAATAATAGCAGATTGTAGTGTCAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ
IGNSHVHSTDDPEAARSSNSKITTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPFVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAG**ATG**ATGGGCTTGG
 GAAACGGGCGTCGAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCTGCATC
 ATCGTCTTTGGGCTTCACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAAATCCAGTCCAGC
 CACAACTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA
 TAACATCACACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
 AGGAAGTTCTCTACGACCTGAGCCAGTGATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTCAACAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCAGGCTGCAG
 GCAGCAGGCCCTGCCACACAGAGGTGCCACAAGGGAAGGGAACCTGCTTGGTAACAGCAA
 GTCCCAGACACCAGCCCCAGTTCCGAAGTGTTTTGGATTCAAAGAGACAAGTTGAGAAAAG
 AGGAAACCAATGAGATCCAGTGTTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGAGGAG
 CCAGGCCGGGAGCAGTGTTGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCTAGTGAGCCAGGAAAATCCAGAGA
 TGGAGGGCCCTGAGCGAGACCAGCTTGTATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT
 GCCGGGGAAGGGAGAAAACAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
 TTTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG
 AATCATACACTC**TGA**ATTGAACTGGAATCACATATTTACAACAGGGCCGAAGAGATGACTA
 TAAAAATGTTATGAGGGACTGAATACTGAAAACCTGTGAAATGTACTAAATAAAATGTACATCTGA

FIGURE 58

MMGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQLQALSEFPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

GGATG CAGAAAGCCTCAGTGTGTGCTCTTCTGGCCTGGGTGCTGCTTCTCTTCTACGCTGGCATTGCCCTCTTCA
CCAGTGGCTTCTGCTCACCGGTTTGGAGCTCACCACCATAGCAGCTGCCAAGAGCCCCAGGCGCTGGGTGCC
TGCCATTGGGGGAGCCAGAGGAAACCTGGGCGCTGCTGGATGGCTTCCCGATTTTTCGGGGTGTGTGTGGTCCGTA
TAGATTGCTTCGGATTGACTTTCGCCCGACGCCAGCATTACACGCTGCCCTAGAGAGCCCTCCTGCTCTCCCTACCTCT
TCCTGGGCAAACTAAGCTCCTTGGCAGGGATCCTGGAGATTTCAGCCGCACTGCCCGGCTCTACCGATCTCAGG
TTGACCTCTTACACCACCATGCGAGCGCTCAAGGCCCTCACCAGTGGCTCTAGCTGCTACCTTTATTGATGCTG
GTAGTAACCTTCGCCACGCCGCTATAGTGGAAAGACAATCTCATTAAGCAGCTCACCAGTGCAGGAAGGGCTGTAG
TCCTTATGGGAGATGATACTTGGAAAGACCTTTTCCCTGGTGCTTTCTCCAAAGCTTTCTTCTTCCCATCTCTTCA
CTCTCAGAGACCTTAGACAGTAGGACAATGGCATCTTGGAAACCTCTACCCCAACCTAGGACAGTGGTGAATGG
ACGTGCTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAGCATGGCCCTCACCACCTGAAATGGCCA
AGAACTTAGCCAGATGGACCAAGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGTGCTCTCTTTCT
TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC
CCACGCTGGCCCTGCTGCTGGGCTGCCATCCCATTTGGGAATATCGGGGAAGTATGGCTGAGCTATTCTCAG
GGGTGAGGACTCCAGCCCCACTCTCTGCTTTAGCCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
CCGATTCTTCTATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCACTCAGCTCAGAGACCTCT
TCTCCAAAGGCTCTGCTGACTACCACTGGCTTCTCCAGAGCCCCAAGGGGCTGAGGGCCAGCTGCCAGCTGTGA
TTGCTGAGCTCAGCAGACTTCTCGGGGGAGCTCGGGCCATSGCATCAGTGTCTGGGCTCGTTTCTCTCTGGTGC
GCATGCGGGGGGTACTGCTGCTCGGGCTGCTTCTGCTTATCTGCTGCTGGCATCTCAGTGGGCATATCC
CAGCGTTCCTTCCATTCTGCCCTCTACTCTGACACCTGTGGCTCGGGGCTGGTGGGGCCATAGGCTATCTCTGGAC
TCTGGGAACCTATGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTCAGTGGCATCTGCTCCCTT
TTCTGTGGAAGGCTCGGGCTGGCTGGGCTCGAGAGGCCCTTGGCAACCTGTTTCCATCCCTGGGCCGCTCC
TGTTACTCTGCTGTTTCGCTTGCTGTGTTCTTCTCTGATAGTTTGTGTAGCTGAGGCGAGGGCCACCCCT
TCCTTTTGGGCTCACTCATCTGCTCTGCTGGTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACTAAGCTAC
TCACAATGCCCGCCTTGGCATTACGCCACAACAAACCCCCACGGCACAAATGGTGATATGCCCTGAGGCTTG
GAATTGGTGTGCTTTATATGACAAGGCTAGCTGGGCTTTTCACTGTTGCCCTGAAGAGCACCTGTTTGGCCACT
CCTCTCCCTGCTGAGTCTCTGGCATCCATGGTGGGTGCTCGAGCCAGAATTTATGGATGAGAGCTTGTGTGG
CGGCGCTGGTGGCCCTGTAGCTGCCGTGCGCTTGTGGCTTCGGCGCTATGGTAATCTCAAGAGCCCCGAGGCCAC
CCATGCTCTTTGTGCGTGGGAGCTGCCCTAATGGCATTGGGTACTGCTGCCACTCAGGACATTGGCGTGGGGG
CAGATGAGGCTCCCCCGCTCTCGGGTCTGGTCTCTGGGCACTCATGGTCTGCTCGGGCTGTAGCAGGGC
TGGCTGCTTCAGGGCTCGCGTGTCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGGCTCCAA
GGACAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAA
TCTACCGACACATGCAGAGGAGATTCCGGGCGCGGTAGAGAGGACCAAAATCTCAGGCTCCCTGACTGTGGGTG
CTTATCAGTTGGGGAGTCTACTCAGCTGCTATGGTCAAGCCCTCACCTGTTGGCTTCCCACTTCTGCTGT
TGCATCGGAGCGCATACCCCTTGTGTTCTGCTTCTGTTTCTGCAAGCTTCTCTCTCAATCTGCTTGTGCTG
CTGGGATACCCGCTACCAACCTGGTCTTTTACTGTGCCATGGCAGGCACTCGGCTTGGGGCCCTCATGGCCA
CACAGAGCTTCTATCTCCACAGGCCACAGGCTGTCTTCCAGGCATCCATTGGCATGCAAGCTTCTGGGATCTCC
CAGAGGCTCATGGCTCCTGTACTTGGCTGCTGCTTTGCTAGTGGGAGCCAAACCTTTCCTCCCACTCTCTCT
TTGCAGTAGGTTGCCACTGCTCTGCTCTGGCCTTTCCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC
CCCCGGAATGAGCTGATGCCAGAGTCAAGCCGAGGAGGAAGAGGAGCACTGATGGAGATCGGGCTCCGGC
ATCGCGCTCAGCACTTCTATGCAAGCACTGCTCAGCTGGGCTCAAGTACCTTTATCCTTGGTATTAGATTCT
TGCGCTGTGCTTGGCAGCTCCATCTTTCGAGGCATCTCATGGTCTGGGAAGTGTTCGCCCTAAGTCAATAT
TGTAGGCTGTGGGCTCATTTGTGAGCAGCGTGGGACTTCTCTGGGCACTAGCTTTGGTGATGAGAGTGGATGGGT
CTGTAGCTCTGCTGTTGAGCAGCTATTCTGGCCAGCAGAGGTAGCCTAGTCTGCTGATTCTGGCACTTGGCT
ACAGAGAGTGTGAGAACAGGTGTAGCTGGCTGTACAGGTAAGTGTGATCTGCAAGCAGGCTCAGCCATAC
TCTTACTACTCATGACAGCGGGCCGCTGACATCTAGGACTTCAATTATCTATAATTCAAGACCAAGTGGAGTA
TGATCCTCAATCTCATATTGGATGCATCTGAGGACAAAGGGGGCGGTCTCCGAAGTGGAAATAAATAGGCCCG
CGTGGTGAATTCGACTATATCCAGCACTTTGGGAGGCAGAGGTGGGAGATGTCTGGTCCGAGAGTCTCA
AGACCAGCTGTGGAACATAACAAGACCCGCTCTCTACTATTTAAAAAAGTGTAAATAAATGATAATAT

FIGURE 60

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFIFYAGIALFTSGFLLTRLELTNHSSCQEPPPGSLPWGSQKPGACW
MASRFSRVVLVIDALRFDAQPPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTMMQRLKALTTGSLPTTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFEMGDDTWKDLF
PGAFSKAFFFPFSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCHGKHGPHHPM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAAFLYSPTAVFPST
PPEEPEVIPPQVSLVPTLALLLGLFIPFGNIGEVMAELFSGGEDSQPHSSALAAQASALHNAQ
QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCICLLASQWAISSPGFFPCPLLLTPVAWGLVGAI
YAGLLGTIELKLDLVLGAVAAVSSFLPFLWKAWAGWSKRPLATLFPPIPGPVLLLLLFLRLA
VFFSDSFVVAEARATPFLGSGFILLVVLHWEQQLLPKLLTMPRLGTSATTNPRHNGAY
ALRLGIGLLLLCTRAGLFHRCPEETPVCHSSPWLSPLASVMVGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVL
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAYQLGSVSYAAMVTALTLLAFPLLLLHAERISLVFLLFLQSF
LLHLLAAGIPVTPGFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAVFVGPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLLPFLCESQGLRKRQPPGNEADARVRPEEEEEP
LMEMLRLDAPQHFYAALLQLGLKYLFIILGIQILACALAASILRRHLMVWVKVFAPKFIIEAVG
FIVSSVGLLLGLIALVMRVDGAVSSWFRQLFLAQQR

```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCGCGTGC GCCCGCGTGTCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT
GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
TCATCACAAATTGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
CCTGACAGTCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAA
TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATTAATAATCAACAGAACGTGGTCC
CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGGGT
ACAGTGGAGTCCCTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAAATCATCTTCTGGTATGTTTTG
CCCATATCTATTACCGTGTCTTTTTCTGTGTGATGGGCTATTCCATCTACCGATATATCCA
GTTTGGCAAGAGAAACACCCAGCAAATTTGATTTTATTTATGAAATGAATTTGACAAA
GATTTCTTTGTGCTGCTGAGAAAAATCGTGATTAACCTTTTACCCTCAATATCTCGGATGAT
TCTAAATTTCTCATCAGGATATGATTTACTGGGAAAAAGCAGTGATGTATCAGCCCTTAA
TGATCCTCAGCCAGCGGGAACCTGAGGCCCTCAGAGGGAAGAGAGGTGAAACATTTAG
GGTATGCTTCGCATTTGATGGAATTTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT
CTCACCCAGCAAGAGTCCCTCAGCAGAACATACCCCCGGATAAAACAGTCATTGAATATGA
ATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG
AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGACGGCAGCGTTGGCAGTCTTGGGCCG
CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
CACAGACTCGAGGAGGGGGCCGGAGGAAGAGCCATCGACACCCTGGTCAGCTGGGATCCCC
AAACTGGCAGGCTGTGTATTCCTTCGCTGTCEAGCTTCGACCAGGATTCAGAGGGCTGCGAG
CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
TCCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTATGAGGAATGGGGGT
TATATGTGCAGATGGAACATGATGCCAACACTTCCTTTTGCTTTTGTTCCTGTGCAAC
AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAGAAGTTTTTCCAGT
TTGTCACTGTCTGTGAGAATTACTTATTTCTTTCTTATTTCTATAGCAGCTGTGTGATTG
GTTCTGATCATGTAGGTCTCTTAACAATGATGGTGGGCCCTCTGGAGTCCAGGGGCTGGCCGGT
TGTCTCATGACAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAAATTTATTCAG
TGGGTGT

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRVFKELKLLTLCSSQIGPPEVALTTDEKSSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHANLILYIGNEFD
KRFFVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDKTVIEYDYVRTTDICAGPEEQELSL
QEEVSTQGTLLSQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDLGEEGLLSRLYEPPADRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
 TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT
 GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
 TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGGCCAAACATCACTGCGGA
 GGCCTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
 CCGCACTGGCCTGGTGGTGTGGGCGCCACGTCTTGAGTACTGCGGAGCCCAACCAGCAGG
 TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCACGCCAACGAC
 ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
 GCCAGGGAGAAGGGCCAGGCCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
 TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGTGGAC
 CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
 TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTTGGTGTGCAGGA
 ACCGGGCTCACGGCCTCGTTTCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC
 GTGTACACGAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC
 CCAGCCCGCCCCCTGCCTGGGACCACCAGGCCCCAGGAGAAGCCCGCT**TGAG**CCACAACCT
 TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
 AAGCCTGATGTTCAAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
 AAGGGCAGAAGCAAACCCAGTAAATGTAACTGACAAAAAAAAAAAAAAAAAAAAAGAA

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSAEPTQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRLLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLTMLCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCGCTGACGCCTGA
 CGCCTGTCCCCGGCCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG
 CAGGCGCCGCGGTGCTGCTCAAGGACTATGTACCCGGTGGGGCTTGCCCCAGCAAGGCCACC
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
 GGAAGTGCCAGGAGAGGAGGCAACATCATCCTGGCTGCCGAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGCAAAGATCATTGAAGAGGAGGAGCGAGT
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT
 TCGAGATGCAGTTTGCGTTAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
 GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG
 CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCATCTTCTGGCTGCTGGTCAAGA
 GCCCCGAGCTGGCCGCCAGCCAGCACATACTGGCCGTGGCGGAGGAAGTGGCGGATGTT
 TCCGGAAGTACTTCGATGGACTCAAACAGAAGGCCCGCCCCGAGGCTGAGGATGAGGA
 GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA
 GGGAGCAGCCCTCCCCAGAT**TAA**CCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
 ACCGAGGACAGCTGTCCGCATGCCCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCAG
 GACTGGCGGCCGCCATGCCCGCAGTAGGTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
 TGTGCACTTGCAGGCCACGTGAGGAGGCCAGCGGTGCCGTGTCGGGAGGGTTCCAAGGTGC
 TCCGTGAAGAGCATGGGAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
 TGTGCATGCATGGTCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTG
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
 GGTGTTTGTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTATCCC
 GAGTTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
 TTGCTGGGACTCCCACCTTCCATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAC
 TTGCTCATT

FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAKDIRGETLNHHVNAHRLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDEGFEMQFGVNLGHFLLTNLLLDKLKASAPSRILNLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGSVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR
```

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGGCTCGGGGGCGACACGTTCTCGGCGCTGAC
 CAGCGTGGCGCGCGCCTTGGCGCCGAGCGCCGCTGCTGGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGTACTTTCTTTTGCAT
 GAGGATTCACAAACCCCTGTGGCTAACCTCTGCTTGCATTTACTCTCATCAAACGCGCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCGAGGTTGCTTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
 ATTCCATGGCTGGAGGAGGCTGTCACTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAA
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTACAGCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACCAAGTGGTAGC
 TGAGGCTGTATCCAGAGGCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
 TATGTACAGCCCTGGGTTCCAGGCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCCAT
 GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCATCCGGAAGGAGGTGATCCACCTGGA
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
 TACCGCATCAGCAAAAGTGCTGGCTGAAGGACACTGTTGACCCAAAAGTGGTGACCCCTCAA
 CCACCGCATTTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC
 AGCCCCCTTACAGAAATGAAGTCAGGAAACCGAGTTGCACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCTGTGGTTAGGA
 ATGCAGCACTGTTTTGGTGGAACTGCAAGGAGTGGTGAAGGGACAGTGACACACTTCAT
 GCTGGCTGTCTGTCTGTTGGGAGATAAGTGGTGGCCAACAGTGGATACATGAGTATGG
 ACAGGAATTCGCGAGACCCTGCAGCTCCAGCCCTGAAGC**TGA**ACTGTTGGCAGAGAGAAGC
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCAGCTTTGTCTGTGCCCTCGCAAAATCAGAGGC
 AAGGGAGAGGTTGTTACCAAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG
 AGTTCAGATACCTCTCTGTGGGAACAGGACATCTCAACAGTCTCAGGTTCCGATCAGTGGGT
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAAGTGGCAATGAGGACACCTGCAAGAG
 GGGCTAGCCTGACTCCCAAGACTTAAAGACTTTCTCCCACTGCCTTCTGCTGCAGCCCAAG
 CAGGAGTGTCCCCCTCCCAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT
 TTTAAGTTGAAAACAACCTTCTTTTCTTTTTGTATGATGGTTTTTAAACAGTCATTAATA
 ATGTTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDFERAAARGDTFSALTSVARALAPERRLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAI PWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMA RNVLKYERLLAESPNHVVAEAVIQRPNI PHLQTRD TYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDLHAGCPVLVGDKWVANKWIEYQGFEFRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAGTTCTGCTCCATCTCAGGAGCCCCGTGCTCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGGCCAAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
 ACGAGCGTGGCTGAGGGACCGAGCCGAGAGCCCCGAGCCCCCGTAACCCGCGCGGGGAG
 CGCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGCTCAAGTTTTCTATTATCATCTATTCCACCGTGTCTGGCTGATTGGGGCCCTGGTCTT
 GTCTGTGGGCATCTATGCAGAGGTGAGCGGCAGAAATATAAAACCCCTGAAAGTGCCCTCC
 TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTGTGTCATGTTTCATGGTCTCCTTCATTGGT
 GTGCTGGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
 ACTTCTGAAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAA
 AACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCTTGGACCCCTGGCCTGTGGGGTGCCCTACA
 CCTGTGCATCAGGAACACGACAGAAAGTTGTCAACACCATGTGTGGCTACAAAATATCGAC
 AAGGAGCGTTTCAGTGTGCGGATGTCTCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
 CTGGTTCATGGACAACCTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
 TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
 ATGCTGCTTGTGCTACCCCAATAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGTCCTGTGTGTAGTCCACGGCCTCTGCCTC
 CCCAGGGAGCAGACCTGGGGCTCCCTAAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT
 GCCACCTGGGGCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
 GAGCTGAGGCTCTGCTCAGGGCCATTTTCATCTCTGGCAGTGCCCTTGGCGGTGGTATTCAA
 GGCAGTTTTGTAGACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTGGC
 CTCTTCTCAGCCTCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGAGCCTA
 GTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC
 TAATCAAAGCTGGTATTTCCCGCATGTCTTATTCTTGCCCTTCCCCAACAGTTTGTAA
 TCAAACAATAAAACATGTTTTGTTTTGTTTTAAAAA

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLESAFLAP
AIIILLLGVVMFMVSFIGVLASLRDNLVLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRGIEYNYDDLDKFNIMDFVQKKFKCCGGEDYRDWSKNQVHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIIYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACCTTGTGCCCCTCTGA
 CACCTGGGAAGATGGCGCGCCCGTGGACCTTCACCTTCTCTGTGGTTTGTGTGGCAGCCACC
 TTGATCCAAGCCACCCTCAGTCCCCTGCACTTCTCATCCTCGGCCCAAAGTCATCAAAGA
 AAAGTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGTGC CGCTGC
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAAACCC
 GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCACATGACGACTGAGGCCAAGCCACCATC
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACAGCTGTGTCCCGTG
 ATCGAGGCTTCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTC
 CCTCAGCATTGACCGCTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTTC
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC
 TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTGAGCCTCATCGTGAGTCA
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTATGGTCTGTGG
 ACTCTGTGCTTCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTCCTCCCA
 GTGAAGCCCTCCGCCCTTTGTTCACCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC
 ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCAGTGTGATTTGGTG
 AAGGCCTTGGGATTGAGGCGAGCTGAGTCTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
 AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
 CAATAAACACTTGCCTGTGAAAAA

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYL
GAKLLDSQKQVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGQDLILNLNLISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSQVPSLVKALGFEEAESSLTKDALVLT¹PASLWKPPSSPVSQ

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

GAGCGAAACATGGCGAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTGCTCATCGTTTGGCAGCTTCCCTCAGGCTCTGCCCAAAGAAAGGAGATGGTGTATCTGA
AAAGGTTAGTACGCTGATGGATGAGCTAACAAAAGACCTGTAATAAGAAATGAATGGAGACA
AGTTCCGTCGCCTTGTGAAAGCGCCACCCAGGAATAACTCCGTTATCGTCAATGTCTCACTGCT
CTCCAACATGCATAGACAGTGTGCTGTTGCAAGCAAGCTGATGAAGAATCCGAGTCTGGC
AAACTCCGGGCATACCTCAGTGCAATCACCACAGGATATTTTGGCATGGTGGATTTTG
ATGAAGGCTCTGATGTAATTTTCAGATGCTAAACATGAAATTCAGTCCAACTTTATCAACATTT
CTCGCAAAAGGGAACCCAAACCGGGGTGATACATATGAGTTACAGTGCGGGTTTTTCAGC
TGAGCAGATGGCCGTTGGATCGCGCAGACAACTGATGTCAAATTTAGAGTGATTAGACCC
CAAAATTTGCTGGTCCCTTATGTTGGGATGCTTTTGGCTGTTATTTGGTGGACATGTGTAT
CTCGAAGAGTAATATGAAATTTCTTTTAAATAAAGCTGGATGGGTTTTTCAGCTTTTTGTG
TTTTGTGCTTGCTATGACATCTGGTCAAAATGTGGAACCATATAAGAGGACCACCATATGCC
ATAAGAATCCCAACCGGACATGTAATATATCCATGGAAGCAGTCAAGCCAGTTTGTGA
GCTGAACACACATGTTTCTTCGTGTTAATGGTGAGTTACCTTAGAATGGTGGCTTTATG
TGAAGTGCTACCTCTGCATCGATATTGGAAGCGAAGATTAATGTGTGTGGCTGGTATTG
GACTGTTGTATTTATCTTCAGTTGGATGCTCTCTAATTTTAGATCTAAATATCATGGCTAC
CCATACAGCTTTCTGATGAGTAAAGGTCCTCAGAGATATATAGACATGGAGTACTGGAA
ATTCGAAAAACGAAATCGTGTGTTTGAAGAGAAAGATGCAACTGTGTATATTTGTATTAC
CTCTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAGAAGATGTGTAGTGCCTTA
ACAAGCAATCCTCTGTCAAAATCTGAGGTATGTGAAATAATATCTCTTAACCTCTCPT
CCGAGTGAACTTTATGAACATTTAATTTAGTACAATTAAGTATATTAAAAATGTAAAA
CTACTACTTTGTTTTAGTTAGAACAAGCTCAAACACTCTTTAGTTAACTTGGTCATCTGAT
TTTTATTTGCCCTTACCAAGATGGGAAAGTAAGTCTGACCAGGTGTTCCACATATGCC
TGTTACAGATAACTACATTAGGAATTCATTTCTAGCTCTCATCTTTGTGTGGATGTGAT
ACTTTACGCATCTTCTCTTTGAGTAGAGAAATATGTGTGATGTGGTCTCTGAAATG
GAACACCATTCTCAGAGCACACGCTAGGCCCTCAGCAAGACAGTTGTTCTCCTCCTCCGT
GCATATTTCTCATCTGCGCTCCAGCTGAGTGTAGAGTGAGACTGCTCTCAAAAAAAGTA
TCTCTAAATACAGGATATAAATTTCTGCTGAGTATGTGTTTAACACTGTGTTATTAGAAA
GATTTTCAGATTCATTCATCTCCTTAGTTTTCTTTAAGGTGACCCATCTGTGATAAAAATA
TAGCTTAGTGTCAAAATCAGTGTAACTTATACATGGCCTAAATTTCTACAAATTAGAGT
TGTGCTATTATTCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
CAGGGCGAGTGACTTACGCTGTAACTCAGCACTTTGGGAGGCCAAGGACGGACGATCAC
GGGTCAGGAGTTTCGAGACCATCTGGCCAACTGGTGAACCCCGTCTCTACTAAAAATAT
AAAAATTAGTGGGTGTGGTGGCAGGACCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
GAGAATCACTGAACTCAGGAGATGGAGTTTCAGTAGGCCGAGATCAGGCCATGCACTCC
AGCTGGCAACGAGCGAGCATCCATCTCAAAAAAAGAAAAA

FIGURE 74

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTNKRPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLMGVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

FIGURE 76

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFDGRLTFHFGSQVVKLPFFINF
MKTRGTSFLNAYTNSPICCPRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVNLIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVSFDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMPGPIKAGLQVSNVSLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

```

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATG
 GCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
 GGTGGCCATGCTGCTCCCCAGCTGGAAAAACAAGTTCTTATGTGCGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCAG
 TGTGACATCTATAGCACCTTCTGGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
 ATCCTTGGAGGCCTCCTGGGATTCAATCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA
 CTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTCTGCTCATCC
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT
 ATGTGTGAAAGAACCAGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
 CACCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
 CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG
 ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCACTCTGTATGACTCCACAGTGTCC
 AGACTAATTTGTGCATGAAGTAAATAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAAATA

FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYYILGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRICTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPIVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

FMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**ATG**GTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTG
TGAAGCTGAAGGTTCAGGGTGTGAATTCCAGTGCCACTCATCTCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCT**TGA**GAGACATAGAAAGAAAATCAACTTTCACTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRI FAPAYVSVCLLLCPREVIAPAGSEPWLCQPA PRCGDKIYNPLEQCCYNDAIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTND FVVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

1000
900
800
700
600
500
400
300
200
100
0

FIGURE 81

CTCCACTGCAACCACCCAGAGCC**ATG**GGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCCA
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAG**TAA**TGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCCTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCCTCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCCTCACCCCT
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM L CQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVC FEQCCPWT FMVKLINQNCDSARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

Figure 82 = "Signal peptide"

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLFLAASLGPVAAFVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ
DSENITAAALATGACIVGILCLPLILLLVYKQQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
 TTCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCTGCCCCTCC
 TTTCTGCCCACCGCTGCTTCTTGGCCCTTCTCCGACCCGCTCTAGACAGCAGACCTCCTGG
 GGTCTGTGGGTGATCTGTGGCCCTGTGCCTCCGTGCTCTTTCTGTCTCCCTTCCTCCCGA
 CTCGCTCCCGGACCAGCGGCTGACCTTGGGGAAAGGATGGTTCCCAGGTGAGGTCCTC
 TCCTCCTTGTCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCCGCC
 AGACATGTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
 TGTTACCGCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAGTCCTGCC
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCACTGCCCATGAGCTGTTCCCTCC
 CGCTGCCCAACCACTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
 AACCTGCCCCGAACAGGCTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC
 CCCCCTGCGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAACCTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
 AAGAGCTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTG
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCGAGT
 ACCCTGCGCTCACCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGGACAAA
 GCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTCTC
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCGCTTGAACACGAGG
 CCTCGGACTTGTTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAG
 GAAGTCACTGGAACGTCTTCTAGCCCAGACCTTGGAGCTGAAGGTACGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTGTT
 ATTATATATTATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSFGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPVHCPQFPVTEPQQCCPKCVPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFP SRLPNQC VLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFREPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWP PRRSLERLPSPDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

FIGURE 88

FIGURE 89

[illegible]

FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLSWGFLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVRVFPWVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCIAKLDPQTLDEQ
QWDTPCPRENAEAAFCGTLVYVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTTCTCTCTTCTCTCTAATCCAT
 CCGTCACCTCTCTGTCTATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTTGGTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCTGTCTTCTGTCTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTTCTTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 AAAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAAATTAC
 TGTGTTGGATGCTGGCCTCTATTGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCTAGTCCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG
 GAAAGGTCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTCTCCAAATTCAGTGGAATAATCCAGGCGGAAGTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAATGTAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAGGTG
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTCACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCTGCATGTCCGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAATCCC
 ATAGTCATCTGCCAGTCAACCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
 AATCCAGAGACAAGCAACAGTGAGTCTCTCTCACAGGCAACCACGCCTTCTCTCCCAGG
 GTGAAATG**TAG**GATGATACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCTATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCAATATATTACACTTTCAGTA
 AAAAAA

FIGURE 92

MALMLSLVLSELLKLGSGQWQVFGPDKPVQALVGEDAAFCFLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFFRPTAKWKGPQGDLSTDSTRNDRMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELEDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRNLNGEHLTYFTLNPRFISVFPRTPTPKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSSESSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGC GCCCGGTGGCGGTGGCGGGCGCGGTTCGCGAGGCTTCCTTGGTCGGATTGCA
 ACGAGGAGAGATGACTGACCAACCGACTGGCTGAATGAAATGAATGGCGGAGCCGAGCGCGC
CATGAGGAGCCTGCCGAGCCTGGCGGCCCTCGCCCTGTTGTGTGCGCGCGCCGCGCGCGCG
 CCGTCGCCTCAGCCGCCTCGGCGGGGAATGTCACCGTGGCGGCGGGGCCGCGGGGCGAGTG
 GACCGCTCGCCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCTTAGGGCGACGGC
 TCCACGGGCCAGGCCCGGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCAGTCCCGGAGACCACCCCTCTTTGGGCGAGTGTGGACCCCTCTTCC
 ACCACCTTTCAGGCGCGCTCGGCCCTCGCGGACCACCCCTCCGGCGCGGAACGCATCTC
 GACCACCTCTCAGGCGCGGACAGACCCGCGCGGACCAACCCCTTCGACGACCACTGGCCCGG
 CGCCGACCAACCCCTGTAGCGACACCGTACCGGCGGCCACGACTCCCGGACCCCGACCCCG
 GATCTCCCGAGCAGCAGCAACAGCAGCGTCTCCCAACCCACCTGCCACCGAGGCCCCCTC
 TTCGCTCCTCCAGAGTATGTATGTAACCTGCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACCTGTGAACCC
 TGCAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAG**CAACAGAGGGTGGAACCTGAAGTTTAT
 TTATTTTAGCAAGGGAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
 GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATCTCTTACTTTTATATGT
 TATATTTAATGTGACGATTTAAAAACATCTAATTACTGATTTAGTCTCTCAAAGCACTAG
 AGTCGCCAATTTTCTCTGGGATAATTTCTGTAATTTTATGGGAAAAAATTATTGAAGAAAT
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT
 ATGTTTATTAATATACCATTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTA
 ATCAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCTAATTTA
 TTTAACTAGTGGTAAAGTAGCTGGTTTACTCTATTTACCAGTACATTTTGGAGCAAAAG
 TAGATTAAGCAGGAATATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA
 ATAATGTACTGTTATCTAAGCATTGTCCTGTACTGCACTGAAAGTAATTTATCTTTGACCT
 TATGTGAGGCACTTGGCTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT
 AATGAAAAAATAATGACAGGTTATACTAGTGTAACCTGGGTATAACCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTTGGGCAAGTAATTTCTTTCACTGAGCTTGTTCCTCTCAAG
 GTTGTGTGAAGATTAATGAGTTGATATATATAAAATGCCATGACATGTCACTCAATAAA
 TTCTGGTTGTTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAATGTTTTAAGA
 ACTTTTAGCTCCTTGACAAGAAGTGCTTTTACTTTAGCACTAAATATTTTAAATGCTTTA
 TAAATGATATTACTGTTATGGAATATTGTATCATATTTGAGTTTATTTAAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGCGGGTGGAT
 CACTTGAGGCCAGAGTTCTAGATGAGCTGGCCAGCACAGTGAACCCCGCTCTACTAAA
 AATACAAAACAAATAGTGGCGTGGTGGCACACCTGTAGTCCGAGCTACTCGGGAGGCT
 GAGGAGGAGAATCGTTGAACCCGGGAGGTGGAGGTTGCACTGAGCTGAGATCGGCCACT
 GCACTCCAGCCTGGTGAGAGAGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSLGLGALLCCAAAAAASASAAGNVTTGGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSSTTFQAPLGFSPTTPPAERTS
TTSQAPTRPAPTTLSTTTGPAPTTFVATTVPAPTTPRTPTPDLPSSSNSVLPTPPATEAPS
SPPPEYVCNCSSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYTSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGG**GATG**GGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
 TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCTGAGCAGCTTCTTGGG
 CCCTGGTACGTGCTTGC GGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
 GAACGTCTGTGGGGGTGGTGGTGACCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
 AGCACGGGCTGGGAGGGTGTGACCAGAGTGT CATGGACCTGATAAAGCGAAACTCCGGATGG
 GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
 CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
 ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC
 CTGGGCTTCTGTACAG**TAG**CAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT
 CCTTCTGTGAGTGTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
 GTGTCCACCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTTC
 CACAGCA

FIGURE 96

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRITLSSQHGLGGCDQSVMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

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FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGAC**ATG**CTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCTACCCCTCGCAT
 GGCTGGATTACCTGGCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
 GCACCTGGAGTCCGGCTGCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCTGTGAGCAG
 GGGACACCCCTATGATCTCTGGATAGGGACCTCCGTGTCCCCCTGGAGCCCTCCACCAC
 CCGCTCCTCGGTGCTCACCCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGGCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC
 CCGCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
 CAGTTGACAGCAATCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
 ATTACCTGCAGAGCTCAGAACCCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGTGGTCGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCTGTCCTTCTGCGTCATCTCTGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTAGCCT
 CTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCAGACCAGCCTCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGATGA**G**AAACTGCAGAGACTCACCCTGATTGAGGGATCACAGCCCTCCAGGCAAGGA
 GAAGTCAGAGGCTGATTCTTGTAGAATTAAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFYPSHGWIYPGPVVHGYWF
 REGANTDQDAPVATNNPARAVWEETRD RFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
 SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTTPMISWIGTSVS
 PLDPSTTRSSVLTLPQPQDHGTS LTCQVTFPGASVTNKTVHLNVSYPPQNLTMTVFQGDG
 TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
 HLRDAAEFTCRAQNPLGSQQVYLVNLSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
 CRKKSARPAAGVGD TGIEDANAVRG SASQGPLEPWAEDSPPDQPPPPASARSSVGE GELQYA
 SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 100

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTFLGLVTLGLAAALSFTLEEEDITGTWYVKAMVVVDKDFPEDRRPRKVS PVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYQLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREAL EEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

Important features:**Signal peptide:**

amino acids 1-17

FIGURE 101

STTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCAC
AGCAGCCAAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA
TCCTGCTTGTCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTGCAG
TGCAAGCCTCACTCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTG
GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCACTGCCTCAAGCCCCGCTACA
TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
ACTGATGCTCTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACACCAGCAATGA
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACTGGGCTGTGCGACCCCTACCC
TCTCTCTACCGTGTGTCTACTGCTGCGACAGCTGCCTCATTTCGCGGTGGGGCAGCAGCTCC
AGCCCCCAGTTTACGCTTGCCTTACACCTTGCAGTATGCGCCAAACATCACCATCATTGAGCACC
GAAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGGCCCTCTGGTCTGTAACAGTCTCTT
CAAGGCATTATCTCTGGGGCCAGGATCCGTGTGCGATACCCGAAAGCCTGGTGTCTACAC
GAAAGTCTGCAAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCA
CCCACCACAGCCCATCACCCTCCATTCCACTTGGTGTTTGGTTCCTGTTCACTCTGTTAAT
AAGAAACCCTAAGCCAAGACCTCTACGAACATCTTTGGGCCTCCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGGTTTCAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA
AAGACAGCTCCTGGCCATATATCAAGTTTCAATAAATATTGCTAAATGAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIKGFCEKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCGISGWSSTSSPQLRLPHTLRCANITIIHQKCNAYPGNITDTM
VCASVQEGGKDCSQGDSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

```

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTTCGTCTGGAGCCG**ATG**CCAAAAACCATGCATTTCTTATTTCAGATTCAATTGTTTT
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACC GAAGAA
GTGAAAATAGAAGTTTTGTCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTTGTTCTTGGTGTTGGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCCCTCATTT
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG
AGATTGAACCTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTAAAGA
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
GAAC**TAG**CATATTTGTATTTCTACTTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTCCCCATGAGAAGATATTTTGA
TCTCCCCAATACATTGATTTTGGTATAATAATGTGAGGCTGTTTGCAAACTTAAAAAAA
AA

FIGURE 104

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFLGVGVQVIKGLDIAMTDMCPGEKRRVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDFKKNDDHGDGFISPKYINVYQHDEL

```

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTCCTGGGATCCCCCTCCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPILLPLGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSRL

Signal peptide:

amino acids 1-18

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FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGGCAC
 AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**
 GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
 CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCC GGCTACCTGGGAGCCTCGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC
 CCCTGCCCTTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
 ATCAACAACCAACCCACGGAACCCATTCCC GGATCTGCTCCAGTGCCCTCAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
 GCGGCGTCCCGGGGCAGGATGCCCTGCCAGGGTGATTCTGGGGGCCCTTGGTGTGTGGGGGA
 GTCTTCAAGGTCTGGTGTCTTGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**TGAC**
 CTGTTTCTCCACCTCCACCCCAACCCCTTAACCTGGGTACCCCTCTGGCCCTCAGAGCACC
 AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTGGCCTGGGAACCTCTTGGAACCTT
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMKELGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRS AVLKLV
MFEGKANESSPKPVGPPPERDIASLP

THESE = GENE

FIGURE 111A

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTTGCCTCCGAGAGGCAGCCTCCTCCA
 GGAGCGGGGCGCTGCACACCATGCGCCCCGGGTGGGCAGGGGTGCGGCCCGCCGCTGCGCGCC
 CGCTTGGCGCTGGCCTTGGCGCTGGCGAGCGTCTGAGTGGGCGCTCCAGCGCTGCGCTGCC
 CACCAAGTGTAACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCTCCGCGCGGTTT
 CTCGGGGGATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC
 ACCAAGATGGATTCGCTGGGCTCAAGAACCTCCGAGTCTTGCACTCTGGAAGACAACCAAGT
 CAGCGTCTATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCTGAACA
 AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA
 GATTGAGTGAAAACCCAGATCCAGGGGATCCCGAGGAAGGCGTTCGCGCGCATCACCGATGT
 GAAGAACCTGCAACTGGACAACAACCATAGCTGCATTGAAGATGGAGCCTTCCGAGGCGC
 TGCGCGATTGGAGATCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGC
 TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
 CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTACACATCT
 GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAGAAGGAGTACGTG
 TGCCCGAGCCCCCACTCGGAGCGCCCATCCTGCAATTGCCAACTCCATCTCTGCCCTTCGCC
 CTCGACCTGCGAGCAATAACATCTGGACTGTGCGAGGAAAGGGCTTGATGGAGATTCTTGCCA
 ACTTGGCGGAGGCGATCGTCGAAATACGCTAGAACAGAACTCCATCAAGGCCATCCCTGCA
 GGAGCCTTCCACCGAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
 TATGCTCCAGATGCTTCCAGGGCCTGAAATCACTACATCCGCTGCTGCTTATGGGAACA
 AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
 AATGCCAACAGATCAACTGCTGCGGGTGAACACGCTTTCAGGACCTCGACAGACCTCAACTT
 GCTCTCCGTGTATGACAACAAGCTGCGAGCCATCAGCAAGGGGCTCTTCGCCCTCTGCGAGT
 CCATCCAGACACTCCACTTAGCCCAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG
 GCGGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCGCGCTGCAGCAGCCGCGCGCG
 ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTGCGCTGCTCAGGCTCCGAGG
 ATTACCGCAGCAGGTTTCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGGAAGTGTGCG
 TGTGAGGGCAGGATTGTGACTGCTCCAACCAGAAGCTGGTCGCATCCCAAGCCACTCCCTCC
 TGAATATGTCAACGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
 TCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCT
 GGAGACCGTGCACGGGCGCGTGTTCGTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA
 GTAACCTGATCAGCTGTGTAGTAATGACACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTG
 TCCCTCTATGACAATCGGATCACCACTACCCCTGGGGCCTTACCACCGCTTGCTCCTCT
 GTCCACCAATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACTGGCCTGGCTCGGCA
 AGTGGTTGAGGAAGAGGGGATCGTCACTGGGAACCTAGGTGCGCAGGAAGCATTTTTCCTC
 AAGGAGATTCCATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAG
 TAGCTGCCAGCTGAGCCCCGCGTGGCCGGAGCAGTGCACTGTATGGAGACAGTGGTGGCAT
 GCAGCAACAAGGGGCTCCCGCGCCTCCCGAGGCGATGCCAAGGATGTGACCCGAGCTGTAC
 CTGGAAGGAACCACTTACAGCGCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGAGCGT
 TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACTTCAGTAACATGCTC
 ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCGCTCCACGCTTCAAC
 GGGCTCGGGTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCTGGAAG
 CTCCTTCAACGACCTCAGATCTCTTCCCATCTGGCGCTGGGAACCAACCACTCCACTGTG
 ACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAAGCGGGGTACAAGGAGCTTGGCATCGCC
 CGCTGCGAGTACGCTGAGGCCATGGCTGACAGGCTCCTGCTCAACCCCAACCCACCGCTT
 CCAGTGCAAGGGGCGCATGACATCAACATTGTGGCCAATGCAATGCTGCTCTCCAGCC
 CGTGCAAGAATAACGGGACATGCAACCAGGACCTGTGGAGCTGTACCGCTGTGCTTCCGCC

TACAGCTACAAGGGCAGGACTGCACCTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
GCATGGAGGACCATGCCACCTGAGTGACAGACCAAGGATGGGTTCAGCTGCTCTGCCCTCT
TGGGCTTTGAGGGGACGGGTGTGAGATCAACCCAGACTGACTGTGAGGACAACGACTGCAGAA
AACATATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCTGAGCTGAACCTCTGTACAGATG
AGGCCAAGTGCATCCCCCTGGACAAAGGATTCAAGTCGAGTGTGTCCCTGGCTACACGGGG
AAGCTCTGTGAGACAGACAATGATGACTGTGTGCCCCAAAGTGGCCCGACGGGGCCCACTGTG
CGTGACACAATCAATGGCTACACATGCACCTGCCCGCCCAAGGGCTCAGTGAACCCCTCTGTG
AACACCCCCCACCCTAGTCTCTACTGCGAGCCAGCCCATGCGACCAGTACGAGTGCCAGAAC
GGGGCCAGTGCATGTGGTGCGACGAGGAGCCCACTGCCGTGCCACAGGGCTTGTCCGGG
CCCCAGTGCAGGAAGCTCATACCTGTCAACTTCGTGGGCAAGAGCTCTCACTGTGAACATGG
CCTCCGCCAACGTTCCGACCCCAAGCCAAACATCTCCCTCGAGTGTGCCATGACAAGGACAA
GGCATCTTCTATCAAAAGGAGACAATGACCCCTGGCATGGAGCTGTACCGAGGCCACGT
GCGGCTGGTCTATGACAGCCCTGAGTTCCCTCCAAACCAAGTGTACAGTGTGGAGACAGTGA
ATGATGGGCAAGTTTCACAGTGTGGAGCTGTGAGCTTAACACAGACCTGAACCTAGTATGTG
GACAAAGGAATCCAAGAGCCTGGGAAGCTGCTCAGAAGCAGCCAGCAGTGGGCATCAACA
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCCTCTCCGCCTTGGCCAGGGGACGG
ACCGCGCTCTAGGCGGCTCCACGGATGCTCATATGAGTGTGCCGATCAACAAACGCTGCGAG
GACTTCAAGCCCTCCACACAGACTCCTGGGGTGTACACAGGCTCAAGCTCTGCACCGT
GTGCAAGCAGCGCCTGTGCCGCTCGTGGAGAGGACGACGCTGGTGTGCGAGTGCGCCACG
GCTGGACCGGCCACTCTGCACAGGAGGAGCCCGGAGCCCTGCCCTGGCCACAGATGCCAC
CATGGAAATGTGTGGAACCTGGGACCTCATACATGTGCAAGTGTGCCAGGGCTATGGAGG
GGACTGTGTGACAAAGAAATGACTCTGCCAATGCTGCTCAGCCTTCAAGTGTCCACATG
GCGAGTGGCATTCTCAGACAAAGGGAGGCCCTACTGCCTGTGCCAGCCGGCTTATGCGCG
GAGCATGGCAACAAGAGAATCCGTGCTGGGCAAGTAGTCCGAGAGGTGATCCGCGGCCA
GAAAGTTATGCAATCATGTGCCACAGCCTCCAAGTGCCCATATGGAATGTCTGTGGGGGCT
GTGGGCCCCAGTGCTGCGAGCCCAACCGCAGCAAGCGCGGGAATACGTCTTCAGTGCACG
GACGGCTCTCTGTTTGTAGAAGAGTGGAGAGACTTAGAGTCCGGCTGCCCTCGGCTGTTC
CTAACGCCCTCGGCCGCTGCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
ATGTGGGACCCCCCTGGTGATTGAGCATGAAGGAATGAAGCTGGAGGAGGAAGTTAAGAGA
AGAGAATTATTAAGTATATTGTAATAATAACAAAAAATAGAACTTAAAAAATAAAAAAAAAA
AAAAAA

FIGURE 112

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKLQVL
 PELLFQSTPKLTRDLSENQIQGIPRKAFRGITDVKNLQLDNNHITSIEDGAFRALRDLEIL
 TLNNNNISIRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRRQRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVC PAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFQYKKLKRIDISKNQTSDIAPDAFQGLKSLTSLVLVYGNKITEIAK
 GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQITISKGLFAPLQSTQTLHL
 AQNPFCVDCCHLKWLDADYLDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEYDRSFS
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRI PSHLPEYVTDLRNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNTDFAGLSSVRLLSLYDNRITITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRKR
 IVSGNPRCQKPFLLKEIPTQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGRL
 ALPRGMPKDVTLEYLEGNHILTAVPRELSALRHLLTLDLSNNSISMLTNYTFSNMSHLSTLIL
 SYNRLRCIPVHAFNGRLSLRVLTLHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLLTPTHRFQCKGPVDINIVAKNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGKDVPTINTCIQNPCQHGGTCHLSDSHKDGFSCSCLPFEGQR
 CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLCQHEAKCIP
 DKGFSCECVPGYSGKLCETDNDCAVHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMV
 LLQTSPCDQYECQNGAQCI VVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS
 VELVTNLQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIEHRINNELQDFKALPPQSLGVS PGCKSCTVCKHGLCRSVEKDSVVECECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKNDSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRQKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA
GACTCAACTGAGAACTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGG**ATGA**AGGCTGCGGGCATTCTGACCCTCATTTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTTCTCGAGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCCTGCCATGTGCGCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAAATTGTTAAAGA
GACACAAGGAATGAACATATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTTCC**TAA**ACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCTCCCAATA
TTCTTTCTCAAACCTGGAGAGGGAAAAATTAAGCTATACTTTTAAGAAAAATAAATATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

115/249

FIGURE 115

CAGGCCATTTGCATCCCACTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAACCTTGTACATGGCTCCC
 CATTGGTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCAGTGTTC
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTTACAGCTGCTGTTTTTAAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCGTATGTCTCTATCCATCTCTAAATGTACCAG
 CTTTGACTCAGTTGTTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTTATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCTGGGAAATGTGGAACATTATCAGGAATTGAAGAAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC
 CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCCTTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCCCTTGGAGT
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCCTTCTCAGAAGCA
 ATAGAAAAGTTTATCCGTGAACCTTCTTAAAGCCACCATTGGGCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTTCCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGT**TAA**TCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC
 CAGTTTTGAAACCAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
 TAAATTTGAATGATACTGTGCCTTAATTGGTTTTCATAGTTTAAAGTGTGTATCATTATCAA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCACAGATTCAAT
 CCACCGAAGTGTTCACTGTCTATCTGTTAGGGAATTTTGTGTCCTGTCTTGGCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTTTTTAAAGATAATTTGTATTTTGCACACTGAGATATAA
 TAAAGGTGTTTATCATAAAAAAAAAAAAAAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEKFKLFTLVSACIPVFRRLARRRKILFYCHFPDLLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRITSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMCCPV
IAVNSGGPLESIDHSVTGFLCEPDVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

117/249

CTCCCTGGGCGGCAGAACCATGTTGGACTTCGGGATCTT
TGGTGGGAGCCGTGCTCTACCTCTATCCGGCTCCAGAC
ACTCCAACCTGAAGAAAAAGATGGTAATCTTCAGATATT
GTTTCTCGTTAATTTCGATGAGAGATATGGGCCCTGTGGT
TCTCGTGGTTAGTTTGGGCACGTGTGATGTACTGAAGCAG
GACCCCTTTTGA AACCATGCTGAAGTCATTATTAAAGGTAT
TGTAAAACCATGAGGAAAAAATTGTATGAAAATGGTGT
TTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
CAGCAGGTGCCCTCAGCCAGCATGCTTGGTTTTCCT
TAATGGGTAGTACATTTGAAGCATGATCAGGAATCATTCG
TTTGGTCTGAGATTGGAAAAGGCTTTCFAGATGGGTAC
AAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
EAAAAGGAAGGAACCTCAGTCAACATATTTTCATTGACTC
TACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
ATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA
AGAGATAAACCAAGTTTTTGGAAATGGTCTGTACTCC
TATTGTCAGCATGTGCTTTGTGAACTGTTCGAACTGCCA
GCTTCAAGATATTGAAGGAAAAAATTGACCGATTATTATT
TGGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
EATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTTCCT
GAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA
AGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
TCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
TCATTGTTAAATTGATTGAGGAAAAACAACCATTTAAAAA
TAAACCAGTATCACTTTGTAAATATAAACACCTATTGTAC

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVS LGTVDLKQHINPNKTSDPFETMLKSLRLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLLLKSEELLDKWLSPETQHVPLSQHMLGFMKSVTQMVMGSTFE
DDQEVIRFQKNHGTWVSEIGKGF LDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILED SMIFSLASCII TAKLCTWAICFLTTS EEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQCEPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGA
 GACCGCCGCCCTTGTCCTCCGAGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTCCTCTCGCTTC
 CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
 ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG
 TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
 GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
 GGCCCTGTCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT
 TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAA
 AAGAAACCTTCT**TGA**TTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
 CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
 TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
 GTGCTTTGTAATAAAATATGTTTGTAGTAACATTAAGACTTATATACAGTTTAGGGGACA
 ATTAAAAAAAAAAAA

FIGURE 119

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

121/249

FIGURE 121

TCCCGGACCCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCGCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCAGCTGGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGA**ACT**TACGGGTGC
CCACTCAGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
ATCGGGTGGCCACACCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCA**ACT**ATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TGA**GGCC
CTGCTGATCCGCACCCCATTCCTCCCCCTCCCATGGCCAAAAACCCACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

123/249

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT
 GACTCGTGCTGCTTCTGTTCTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCTCTCCGGCTCAGAGGACCTTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCCTCGGAAGCGGGGCCACATCTACCTAAGTCCCGCCCATGGCCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCAGGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTATC
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATC
 TGGG**TGA**CCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGTTGGGCCTCAGGCAGGGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCTCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCTTAGGAGCCAGTCAGCAGGGTGGGGTGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGCGCCCTGAGCCCTTGTCTGTGTCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC
 ACAGCCCATCCGCGTGTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACACCGGGTTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGTGGGGCGGGCCGGCCGAGA
 GCATGTGCTGGATCTGTTCTGTGTCTGTCTGTGTGGTGGGGGAGGGGAGGGAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGAGCAGGAATAAAGCTT
 GCCCCGGGGCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPKICSRDHAQSSATWSCSQPFKVVVCYIIAFYSTDYRLVQKVCPCDYNHSDTPY
YPSG

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA
GGCAGGGCTGATTCCTTGGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTTAAAG
GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
TGGTGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTGACCTAGCCGCTAG
CATCTTCCCAGAGCACC GGATCCC GGGGTAGGAGGCAGCGGGCGAGCACCAGCGCCAGCC
GGCTGCGGCTGCCACACGGCTCACCATGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
GCCGTGCTGCTGGTCCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC
CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
GCTCCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCTTCTCG
GCGGTGCGGAGCACCACACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
CGATCAGATCCTGGTGAATGTGGGTAATTTTTACATTGGAGTCTGTCTTTGTAGCACCAA
GAAAAGGAATTTACAGTTTCAGTTTTACGTGATTAAGTCTACCAGAGCCAACTATCCAG
GTTAACTTGTATGTTAAATGGAAAACAGTAATATCTGCCTTTGCGGGGACAAAGATGTTAC
TCGTGAAGCTGCCACGAATGGTGTCTGCTTACCTAGATAAAGAGGATAAGGTTTACCTAA
AACTGGAGAAAGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTTCTGGTG
TTCCCCCTATAGCATTCAATTTCTCCATGATGTTATCCAGGTGAGGGATGACCCACTCTCG
AGTTATTGGAAGATCATTTTTTTCATATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCAATTCCTGGGATTACTGAATTAGT
TACAGATGTGGAATTTTATTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
AAACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTGTTCTTGTA
AAAACCTGGATTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
TGGCTTGCCACAAAATTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAA
GAATGCTTCATAGTTGATTTTTAATTGTATATGTGAAAGAGTCATATTTCCAAGTTATATT
TTCCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAAAGTTGCTTACCCAAAATCTAAG
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTATACTTTATTGCT
TCAACTTTAATTAATAATGATTGATAATAACCACCTTTATTAAAAACCTAAGGTTTTTTTTT
TCCGTAGACATGACCACTTTATTAACGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA
TATATTTATCTGTTTAGCTAATATTAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTTATTATGTCTGTTATAGAATAAAGA
TTAATATATGTTAAAAAA

FIGURE 126

MSGRRALSAPVAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVFVAPRKGIYSFSF
HVIKVIYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

127/249

FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCCTGCGCTC
 GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCTCATCGCCGGAGC
 TTTCTTCTGGTTGGTGTCTCTACTGATTTCTGTCCTTGTGGTTCATGGCAAGAGTCATTA
 TTGACAACAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
 TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
 GAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
 TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG
 CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC
 GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA
 AAAAGTGGGGCATCCTCCTTATCGTTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
 ATAAGTTCCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGCATGGGCAC
 CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAACTCTGCCTGCTCTGCCAAG
 ACAAGAACTTTCTTTTACAACCAGCGCTCCAGATAACCTCAGGGAACCAGCACTTCCCAA
 ACCGCAGACTACATCTTTAGGAAGCACAACCTGTGCCTTTTTCTGAAAATCCCTTTTTCTG
 GTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 128

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGP TQKYLLIFGAFVS VYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGP TGVGIHGDS PQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAF LAAGGSCRS LKCLLCQDKN
FLLYNQRSR

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAAGCGCGCGCCACCACCGCTGCCATGCGGCCCTGCCGGGGC**CAGT**TTGCTCTGGGCTTGCCCTTCT
 TGGTGTCTCTGGTGGCTCGGTGCAGAGGCATCTGGGGGTTCTGGGGCCCAAGAACGCTCGCGAAGAACGCGCG
 AGTTTGGAGCGCATAGTGGGACAGGTCAACAGCGAGCTGGTCAACATCTACACTTCAACCATCTGTACCC
 GCACAGGACAGAGGGCGGTGCGTGTGTCTGAACGTCCTGAACAGCAGAGGGGGCGCGTGTCTGTTTGTGG
 TCGCCAGAGAGGCTGTGGTGTCTTCCAGTGGCCCTAATCCTGGAGGAGATGTTTACGCGAAGTACCTCT
 ACCAAAAAGTGGAAAGAACCCCTGTGTGAGCCCCCACCAGAATGAGTCGGAGATTCAAGTCTTCTACGTGGATG
 TGTCCACCTCTGACAGTCAACACCAATACCAGCTCCGGGTGAGCCGCATGGACGATTTTGTGCTCAGGACTG
 GGGAGCAGTTGAGTCTCAATACCACAGCAGCAGCGCCAGTACTTCAAGTATGAGTTCCTGAAAGCGCTGGACT
 CGGTAATTGTCAAGGTGACCTCCACAGGGCTTCCCTGCTCAGTCTCATCTCCATTCAAGATGTGCTGTGCTCCT
 TCTATGACTGGACAAACAGTACGCTTATGCTGGTGGTGGTGAAGACCAAGACCAAGCTCGGGGGCT
 AGCGCAAGGACTTCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCAAGACCAAGCTCGGGGGCT
 CCCTGCTTTTCAACCCCTTCGCAGAGATGAACCGGTGATCAAGGGCACCGCCAGAAAAACCTGTGAGTGTCTG
 TGTCTCAAGCAGTCAAGTCTGAGGCATACGTGAGTGGATGCTCTTTGCTGGGTATATTCTCTCCTTTTACC
 TGTGACCGTCTCTGCTGCTGGGAACTGGAGGCAGAGAAAGACCTGCTGCTGGCCATTGACCGAG
 CCTGCCAGAAAGCGGTACCTCGAGTCTGGCTGATTCTTTCTGGCAGTTCCCTTATGAGGTTACAAC
 ATGGCTCCTTTGAGATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCATTGGGACCTCTCTTACG
 GTTACAGGGCCGCTCCTTTGAACCTGTAGGTACTGGCCCGGAGTGGACTCCATGAGTCTGTGGAGGAGGATG
 ACTACGACACATTTGACCGCATCTGATTCCGACAGAAATGTCATTGCGAACCAACATACCTCTATGTGGCTGACC
 TGGCAGCGAAGGACAAGCGTCTTCTGCGGAAAGTACAGATCTACTTGGAAAGTGGCCACTTGGCTGTCTCT
 TCTATGCCCTTCTGTGGTGCAGCTGTGATCACTACCAGACGGTGGTGAATGCACAGGAATGACAGCATCT
 GCTACTACACTTCTCTCGGCCCAACCCATGGGCAATCTCAGCGCTTCAACAACTCCTACGACATCTGGGT
 ACATCTGCTGGGGCTGCTTTCTGCTCATCATCTGCAAGCGGAGATCAACCAACCGCGCCCTGCTCGCGCA
 ATGACTCTGTGCGCTGGATGTGGGATCCCAACACTTTGGGCTTTCTACGCCATGCGACCGCTGATGA
 TGGAGGGCTGCTCAGTCTTGCTATCATGTGTGCCCACTATACCAATTTCCAGTTTGACACATCTTATGAT
 ACATGATCGCGGACTCTGACGTCTGAAGCTCTACAGAGCGGACCGGACATCAACCGCAGCGCTTACAGTG
 CCTACGCTGCTGGGCTTGTATCTCTTCTCTGCTGGGCTGGTCTTGGCAGAGGAAACCGGCTTCT
 GGATCTGCTTCTCCATCTTACATCATGCGCACCTGCTCTTACGACCGCAGCTCTATTACATGGGCGGTGGA
 AACTGGACTCGGGGATCTTCGCGCGCATCTCCAGCTGCTCTACAGACTGCATCCGCGAGTCAGCGGGGCCG
 TCTACGTGGACCGCATGGTGTGCTGGTGCATGGGCAACGTCATCAACACTGGTCTGCTGGCTGCTTATGGGCTTATCA
 TGGCGCCCAATGATTTGCTCTTCTTCTTCTTGGCCATTGGCATCTGCAACCTGCTCCTTTACTTTGCGCTTTACGA
 TCTATCATGAAGCTCCGGAGTGGGAGAGGATCAAGCTCATCCCTGCTCTGCTATGTTTGAACCTCCGTGGTCT
 GGGGCTTCGGCTCTTCTTCTTCTTCCAGGACTCAGCACCTGGCAGAAAAACCCCTGCGAGAGTCAGGGAGCACA
 ACCGGGAGTGCATCTCCTCGACTTCTTTGACGACACGACATCTGGCACTTCTCTCTCTCATGCGCATGTTCG
 GCTCTTCTGGTGTGTGATCATGTGATGACGACTGGATGTCGAGCAGGACAGGCTAGCTTACGTTAGGCTTGGCT
 GTGGGATGAGTCCAGCACCGCTGCCAGCACTGGATGGCAGCAGGACAGCGCTAGCTTACGTTAGGCTTGGCT
 GGGACAGCCATGGGCTGGCATGGAACCTTGCAGTGCCTCTGCCAGGAGCAGGCTGCTCCCTGGAACCCCC
 AGATGTTGGCCAAATTGCTGCTTTCTTCTCAGTGTGGGGCTTCCATGGGCGCTGCTCCTTTGGCTCTCCATTT
 GTCCTTTGCAAGAGGAAGGATGGAAGGACACCTCCCATTTTATGCTGCTATTTTGGCGGCTCCTCCTCCCG
 ACATGCCCGAGCTGGGACCTAAGCGCTCTTTTCTCCTCCTATCCCATCCAGGGCTAGTCTGGGGCTGA
 ATCTCTGTCTGTATCAGGGCCCCAGTTCTTCTTTGGGCTGTCCTGGCTGCCATCACTGCCCATTCAGTCAGCG
 AGGATGGATGGGGTATGAGATTTTGGGGGTTGGGCTGGTGCCAGACTTTTGGTGTAGGCTGCAAGGGG
 CTGGGGAGCTGCGTATTCTCTTCCCTCTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCAAATT
 TGAAGACCGCTCTGATTCAAGAGGCTGAATCAGAGGTCACTCTTCATCCATCAGCTCCCGACTGATGCG
 AGCACCAGGACTGAGGGAGAGGCGCTCACCCCTTCCCTTCTTCTTCCAGGCCCTTAGTCTTGCAAAACCCC
 AGCTGGGGCCCTTTCAGTGCCATTGACACTGCCAAGAATGTCCAGGGGCAAGGAGGAGTATACAGAGTTTCAG
 CCGGTCTGCTCTCCAGCTGTGGGACCCAGTGCCTACCTTAGAAAGGGGCTCAGGAGGAGTGTGCTGTTT
 CCCTCTACGTGCCCTGCTGATCCCTCTGCTCCACCTGTCAGCCAGATGTGAGTTTCCGTCAAGTCTCCAGTCA
 AGTTTCTGTTTAGTCTGACACACATACCTATGAACCTTGGAGTTTCAAAAGAATGGCCAGCTCTGGGCA
 CTGGGCGCCCTGCTGCTGATCCCTCTGCTCCACCTGTCAGCCAGATGTGAGGATGGGAGCTCAGG
 CGGGGCTCTGCTTTGGGAGTGGGAATGTGTTTCTCCCAAACCTGTTTATAGCTCTGCTTGAAGGGCTGGG
 AGATAGGCTGGGTGCTGATCTTCTTCCAGAGCTCTCATGCTATGGTTCATTTCCGTTTCTATGAATGAAT
 TGCATTCAATAAACACCGACTCAAAAAAAAAAAAAA

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESH LGVLGPKNV SQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKGKGA PLLFVVRQKEAVVS FQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRGTGEQFSFNTTAAQPYFKYEFPEGVD SVI
VKVTSNKAFFPCSVISIQDVLCPVYDL DNNVAFIGMYQTMTKKAITVQRKDFPSNSFYVVVV
VKTEDQACGGS LPFYPAEDEPVDQGH RQKTL SVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLLVAIDRACPE SGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGT RPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFWNIIATIA VFYALPVVQLVITYQTVVNVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGIYILLGLLFLLI ILQREINHNRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVC PNNTNFQFDT SFMYM IAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKNTAFWIVFSIIHIIAT LLLSTQLYLMGRWKLD SGIFRRILHVLVYTD CIRQCSG
PLYVDRMVLLVMGNVINWSLAAY GLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFQGL STWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF
```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCTTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTTGGGCGCTGGAGGGCCTGTCCTG
 ACC**ATGGT**TCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC
 CCAGCCTGCGAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAATTTCCCTTTATACC
 TGACCAAGTGTGCCGTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGTCAGGGGACTCA
 GGCAAGGCCAAGTGAAGGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTGACAG
 GGCCTTGACCAGAGAGAGAGAGGAGGAGTACCAAGCTACAGGTACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCTGGCATCCC
 CTTCTCTTCTTGTAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
 TCCACATCTGAGCCAGGCTCCAGCCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCCTCAGGCCACCAGGCCACTG
 CCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCCATATCCCGCCACCACATGGCCCCAGGTACACTGGAGTGGGGTGATGT
 GCACTATCACCTGAGAGGCCATCCCCCGGACCCCTTGAAGTGAATGCAGAGGGAACCTCT
 ACGTGACCAGAGCTGGACAGAGAAGCCACAGGCTGAGTACCTGCTCCAGGTGGCGGCTCAG
 AATTCCTTGGCCAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGTGATGGATGAGAA
 TGACAACGTGCTATCTGCCTCCCCGTGACCCACAGTCAGATCCTCAGCTCAGTCCAC
 CAGGTACTGAAGTGACTAGACTGTGACAGAGGATGCAGATGCCCCCGGCTCCCCAATTCC
 CACGTTGTGATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
 GGTGGACCCCACTTCAGGCACTGTGACGCTGGGGGTGCTCCCATCCGAGCAGGCCAGAAC
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCCGAGAGGGTGGCTTCAGCAGCAGCTGT
 CAAGTCGAAGTCCGAGTCACAGATATCAATGATCAGCCCTGAGTTTCATCACTTCCAGAT
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTAGACTCAGACTCTGC
 AAAGCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGGGA
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCATCAGTGCCCC
 AGCCGGCTCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCT
 CCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAATCTCCGGGGAGGTGCACACC
 GCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCAGGA
 TACAGCCCTGACTCTTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG
 GCTTGATCGTGAAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGGCAAGCTCCCTACAGC
 TTCACCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTTC
 CCATGCTACCTCACCTTGCCCTGCATTGGTGGAGCCAGCTGAACACTAATCCCCGTGG
 TGGTGCCGCAATGCCCCAGATGTGGCAGCTCTGGTTCGAGTATCGTGTGCTCGCTGCAAC
 GTGGAGGGGCACTGTGATGCCCAAGGTGGGCGCATGAAGGGCATGCCACCAAGAGCTGTCCGC
 AGTGGGCATTCCTGTAGGCAACCTGGTAGCAATAGGAATCTTCTCATCTATTTTCAACCC
 ACTGGACCATGTCAAGGAAGAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG
 ACTGTCTGAATGGCCAGGAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCCC
 CTGGAGAGAGCCAGCACCCAAAGATCCAGCAGGGGACAGGACAGTAGAGAAGCCCTCAGC
 CTGCCCTGGGGTGGAGGACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC
 TTTATGGACTGCCATGGGAGTGCTCCAAATGTCAAGGTGTTTGCCCAATAATAAGCCCCA
 GAGAACTGGGCTGGGCGATTTGGGAAAAA

FIGURE 132

MVPAWLWLLCVSVFQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAQYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDGDAQSGHQATATVEVSIESTWVSLEPIHLAE
 NLKVLYPHMAQVHWSSGDVHYHLESHPPGPFVNAEGLYVTRELDREAQAQYLLQVRAQN
 SHGEDYAAPLELHVLMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
 VVYQLLSPEPEDGVEGRAFOVDPTSGSVTLGVLPLRAGONILLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADALEPAFRLMDFAIERGDTE
 GTFGLDWEPPDSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERV
 MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPIRSLRFLVNDSEGWLCIEKFSGEVHTA
 QSLQGAQPGDTYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGPNFTVQRDWRLQTLNGSHAYLTALHWVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGTLVAIIGIFLILIFTHWTMSRKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTTGAGTCAACTAGTGTGAATTCAAAACAACCTTGAAGCTCAATTTCTGGAATCTCCCTCCTCCT
 TCAATCGGCTGTGGATGTCTTGGTCCCATCTGTCACTGTGACGGCATTAAATCCTTCTCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCCCTTTAGACAATGA
 AGATGATGAAATGCAACACATGAGGGGCAAGAACGGAGCAGTAATAACTTCAACTCAGCTCGGG
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTCTGTTGAAAACCGGCCGATGTATGTACTGAAGTT
 CAGCATGGGAAAGCGGTGAGGCGGCCGGCCGTTTTGGCTGAATGCAGGCATCCATTCCCGAG
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTGCTGTGGCCAATCC
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGTCCCGAAATC
 CTGGAAGCTCTGTCATTGGTGCTGACCCAAAATAGAAACTGGAACGCTAGTTTTGACAGGAAG
 GGAGCCAGCGACAACCTTGTCTCCGAAGTGTAACCATGGACCCACGCCAATTCCGGAAGTGGA
 GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCAGCTCGC
 ACAGCTACTCGCAGCTGTGTATGATATCCATATGGGTACTCAGTCAAAAGGCCCGCAGATGCC
 GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTGCGGCACTGA
 GTACCAAGTGGGTGCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGATCGACTGGG
 CGTATGACAAAGGCATCAAAATTGCAATTACCATTTGAGTTGAGAGATACCGGACCTATGCG
 TTCCTCCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACTCTACTAGCGCATGGCTCTGTCTGTCTACATTTAT
 TTGTACCCACACGTGCACGCCTGAGGCCATTGTTAAAGGAGCTTTTCCCTACCTGTGTGAG
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGCTCTGGCGGTGCTCCTGCAAGAACTGGTCTGCCAGCCTGCTCAATTTTGGTCCCTG
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGTGCTGGCGGCTGCACCTC
 AGCATCACCCCTTCTCTGGGTGGCATGTCTCTCTCTACCTCATTTTTAGAACCAAAGAACATC
 TGAGATGATTCTCTACCTCATCCACATCTAGCCAAGCCAGTGACCTTGTCTGGTGGCACT
 GTGGGAGACACCCTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCCCTTTAATTTT
 TCGCAGTCTTCTCGGAAAATATTTTCCCTTTGAGCAGCAAATCTTTGAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCCTCCTGTTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTGTCTTTGTGGC
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTACCCACAACCTCTGCCTCCTGGGTTCAAGCA
 ATTCCTCTGCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCCTGGCTGCTA
 ATTTTGTGTTTTTGTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGTGGGATTACAGGTGTGAGCCACTG
 TCCCGGGCCCGTCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCCTTAC
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCTCTCTTCCCTTTGTTATTACGTGTG
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCAAAATGAGGATGGTGAATATCCCATCTGTCTTAATGGGCTTACCTCCT
 CTTTGCCTTTTGAACCTCACTTCAAGATCTAGGCCTCATCTTACAGGTCTTAATCACTCAT
 CTGGCCTGATACTCACTGCTGCCCTGGCACATTCCCATTTGTGCTGGTGTATCTGTGTGT
 TCCTTGTCTCGTTTGT
 TCTGTCTATTTTGTATCTTGACCACAAGTTCTCAAGTAGAGCAGAATTCATCAACCAGCT
 GCCTCTGTGTTCATTTCACTCAGCACGTACCATCTGTCTTTTGTGTGTGTGTGTGTGTGT
 TTGTTTTTTTGTCTTTTACCAACATGTCTGTAAATCTTAACCTCTGCCTAGGATTTGTACA
 GCATCTGGTGTGTGCTTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFRLRSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNFGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRPPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPATISILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEKSVVDFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDNLV

Signal peptide:

amino acids 1-16

FIGURE 135

[illegible]

FIGURE 136

MASYLYGVLFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGGLGNLTHTPESAIIHQGFQHLVHSLTVP
SKDLTLKMGSA LFVKKELQLQANFLGNVKRLYEAEVFSTDFSNP SIAQARINSHVKKKTQ GK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDVAFFVFLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSVFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

FIGURE 137

GGCTGACCGTGCTACATTGCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGC
 CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCAGCGTCTTGGGAAGCACCAG
 CCTTTATCTCTTCAACCTCAAGTCCCCTTTCTCAAGAACTCTCTGTTCTTTGCCCTCTAAAG
 TCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGGCCACAAAGAGACAGATGAAGATGC
 AGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTC
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC
 CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCA
 GCGTGACCTCCAATGGGGTCAGCATAGTCACCAACTCTGAGTTCATACAACTCCAGTGGG
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA
 CTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC
 CCTCCAGTGGGGCCAGCACAGTCACCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGC
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA
 GTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCA
 GTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCC
 ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG
 CACAACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGGG
 CTGGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCCAGCACAGCCACCAAC
 TCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGC
 TCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCCAGCACAGC
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGC
 ACAACCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGC
 TAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTAGGGCCAGCACAGCCACCAACT
 CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACT
 TCCAGTGGGGCCACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGAGGCTCTGGAAC
 AGCAGCTCTGACTGGAATGCACAACTTCCCATAGTGCATCTACTGCAGTGAAGTGAAGCAA
 AGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCG
 GCCGTGGGGCTCTTGTCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACAC
 CTTTAAACAGCTGTCTACCACTCATGGCTCAACCATGGCTTGGTCCAGGCCCTGGAG
 GGAATCATGGAGCCCCCAGGCCAGGTGGAGTCTTAAGTGGTTCTGGAGGAGAGCAGTA
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGGCCCTGAGCAGCCCCGAAGCAAG
 TGCCGATCTCTCAGGAAGGAAGAGACCTGGGCACCCAAGACCTGGTTTCCTTTCAATCATC
 CCAGGAGACCTCTCCAGCTTTGTTTGGATCCTGAAATCTTGAAGAAGGTATCTCACC
 TTTCTTGCCTTTACCAGACACTGGAAGAGAATACTATATTGCTCATTTAGCTAAGAAATAA
 ATACATCTCATCTAACACACAGCAAAAGAGAAGCTGTGCTTGGCCCCGGGGTGGGTATCTAG
 CTCTGAGATGAACCTCAGTTATAGGAGAAACCTCCATGGCTGACCTCCATCTGGCATTCAAA
 TCTCCACAGTAAATCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAA

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTANTGSSVISSGASTATNSGSSVTSSGVSTATI
 SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTSSGASTATNSE
 SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
 TTSSGASTATNSESSTSSGASTATNSESSTVSSRASTATNSESSTSSGASTATNSESRTT
 SNGAGTATNSESSTSSGASTATNSDSSTVSSGASTATNSESSTSSGASTATNSESSTSS
 GASTATNSDSSSTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTSSGA
 NTATNSESSTVSSGASTATNSESSTSSGVSTATNSESSTSSGASTATNSDSSSTTSSEAST
 ATNSESSTVSSGISTVTNSESSTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
 SEAKPGGSLVPWEIFLITLVSVVAAGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
 GPGGNHGAPHRPRWSPNWFWRPVS SIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
 CCAGCAAT**ATG**CATCTTGACGCTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
 CTGTCTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGC
 ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGAAGCTTAGCAACATGGGGAGCCACACCGGC
 AAGGAGTTGGACAAAGCGCTCCAGGGGCTCAACACGGCATGGACAAGGTTGCCCATGAGAT
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTCCACACTGGGGTCCAC
 CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCAACCATGCTGCTGGCCAGGCCGGGAAGGAGC
 TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCAGCCGTTAGCCTCTGG
 GGCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
 TGCCCT**TAA**ATGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGAC
 ATGACCTGGAGGGGTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG
 GGATTGTGAATAAACTTGATACACCA

FIGURE 140

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSGHTGKELDKGVQGLNHGMDKVAHEINHIGQAGKEAEKLGHVNNAAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 141

CTCCGGGTCCCAGGGGCTGCGCCGGCCGGCTGGCAAGGGGACGAGTCAGTGGCACTCCAGGAAGAGCGGC
 CC CGCGGGGGGCGATGACCGTGCCTGACCTGACTCACTCCAGGTCCGAGGCGGGGGCCCGGGGGCGACTCG
 GGGGCGGACCGCGGGGCGAGCTGCCGCCGTGACTCGCGGAGCCACTGAGCCCGAGCGGGGACACCGCTG
 GCTCTGCTCTCTCCGAAGTCGCGCACCCGCGATGGGCTTGAGGAGCTGCTCGCCGCCCATCTGGGGCGGCTGCGC
 CCTCGGCCACCGCTGCTGCTCTGCTCTGCTGCTGCTGCTGCTGCGACGCGCGCGCTCCGACCTGGGCGCTCAGC
 CCCC GGATCAGCCTGCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGAGAGCTGAACACATCTCCAATAC
 ACAGCCCTCTGCTGAGCAGGGATGGCAGGACCTGTACGTGGTGCTCGAGAGGCCCTCTTTGCATCTCAGTAC
 AACCTCAGCTCTCTGCCAGCGGGGAGTACAGGAGCTGCTTTGGGGTGAGACGCGAGAGAGAAACAGCAGTGC
 AGCTCTCAAGGCAAGGACCAAGCGCGACTGTCAAAACTACATCAAGATCCTCTGCCCTCAGCGGAGCTCAC
 CTGTTCACTGTGGCAGCAGCCTTCAGCCCATGTGTACCTACATCAACTGGAGAATTCACCTTGGCAAGG
 GACGAGAAGGGGAATGTCTCTCTGAAGATGGCAAGGGCCGTTGCTCTTCGACCCGAAATTCAGTCCACTGCC
 CTGGTGGTGTATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC
 CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCTCAGCGTAC
 ATTCTGAGAGCCTGGGCGAGCTTGAAGGCGATGTATGACAGATCTACTTTTCTTCAGCGAGACTGGCCAGGAA
 TTTGAGTTCTTTGAGAACCACTTGTGTCCGCAATGCCCCGATCTGCAAGGGCGATGAGGTTGGAGAGCGGGTG
 CTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCAGCGCCCGACGATGGCTTCCCTTCAAC
 GTGCTCGAGGATGTCTTCAGCTGAGCCCGACGCCCGCAGGACTGGCTGACACCCCTTTCTATGGGCTTCTCACT
 TCCCACTGGCAGCGGGAATCAGAAGGCTCTGCCGTCTGTGCTCTTCAACAATGAAGATGTGCAGAGAGCTTTC
 AGCGGCTCTACAGAGGTGACCTGAGCAGCAGCAGTGGTACACCTGACCCCGCCCGGTGCCACACCCGGC
 CCTGGAGGCTGATCAACCAAGTGCOCGGGAAGGAAGATCAACTCACTCCCTGCACTCCAGACCGCGCTGCTG
 AACTCTCTCAAGGACCACTTCTGATGTGACGAGCGGCGAGGTCCGAAGCGCATCTGAGGAGCTGCAGATCTTCTATCGGA
 TACCACGCGGTGCTGTACACCGCTCCCTGGCTGACACCACTACGATGTCTCTCTCTGGGCACTGTGTGAC
 GGCGGCTCCACAAGCAGTGGGCTGGGCGCCGGTGACATCACTGAGGAGCTGCAGATCTTCTATCGGA
 CAGCCGTCGAGATCTGCTCTGGACACCCACAGGGGCTGCTGTATGGCGGCTCAGACTCGGGCGTATCTCAG
 TGCCCATGAGCCACTCGACGCTGTACCGGAGCTGTGGGGAGTGTCTCTCGCCCGGACCCCTACTGTGCTTGG
 AGCGGCTCCAGCTCGAGCAGCTCAGCTCTACACGCTCAGCTGGCCACCGCGCTGGATCCAGGAGCATCGAG
 GGAGCCAGCGCAAGGACCTTTGACAGCGGTCTTGGTTGTGTCCCGCTCTTTGTATCAACAGGGGAGAGCCA
 TGTGAGCAAGTCCAGTTCCAGGCCAACACAGTGAACACTTGGCGTGCCGCTCTTCTCCAACTCAGCGGACCCGA
 CTCTGGCTACGCAACGGGGCCCCGCTCAATGCTCGGCTCTTGCACGCTGTACCCACTGGGAGCTCTGCTGCTG
 GTGGGACCCCAACAGCTGGGGAGTTCCAGTGTGTTCACTAGAGGAGGGCTTCAGCAGCTGGTAGCCAGGTAC
 TGCCAGAGGTGGTGGAGGACGGGTTGCCAGACCAACAGATGAGGTTGGCAGTGTACCCGCTATTATCAGCACA
 TC GCTGTGAGTGCACCACTGTTGGCAAGGCCAGCTGGGTTGCAGACAGTCTCTACTGGAAGGAGTTCTGTTG
 ATGTGACAGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTATCTTGTCTACCGGCAACCGGAACAGATGAAA
 GTCTTCTGAAGCAGGGGGAATGTGCCAGCTGCACCCCAAGACCTGCCCTGCTGCGCCCTGAGACCCGCG
 CCACTCAAGCGCTAGGGCCCCCTAGCACCCGCTGATCACCAGGGTACCACTCCTGTGCAGACAGCCCCCG
 GGGGCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTCTGTGGAGGTATCTTCAAGT
 TGCCCCCGGCCCGGGTCCGCTTTGGCTCGAGATCCGTGACTCTGTGGTGTGAGGCTGACTTTCAGAGGACGC
 TGCCGTGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGAOCTCCCTCGCTCTGTCTCTTCGTGGAAC
 ACGACCGTGGTGCCCGGCCCTTGGGAGCCTTGGAGCAGCTGGCTGCTGCTCTCCAGTCAAGTACGAGGCTCC
 TACCACCGACACCCAAACAGCCGTTGCCCCAGAGGTCTGGCCAAATATGGGGGCTGCTAGGTTGGTGAA
 CAGTGCTCTTATGTAACCTGAGCCCTTTGTTTAAAAAAACAAATTCAAATGTGAAACTAGAAATGAGAGGGAAGAG
 ATAGCATGGCATGCAGCACACACCGCTGCTCAGTCTCATGGCTCAGCGGGGTGCTGGGATGCTTCCAAAGTGG
 TTTCTGAGACAGAGTTGGAACCTCACCACTGGCTCTTCACTTCCACATTATCCGCTGCCACCGCTGC
 CTGCTCACTGCGAGTACAGGACAGCTTGGGCTGCGTGCTTGTGCTTGGCAGTCAAGCGAGGATGTAGTTG
 TTGCTGCGCTGCTCCACCACTCAGGACAGAGGGCTAGGTTGGCAGTGGCGGCTTCAAGGCTTGGGCTG
 GGACCAACTCTGGACCTTTCCAGCTGTATCAGGCTTGGGCCACGAGAGGAGCAGCGGAGCTCAGGAGAGA
 TTTCTGTAAGTGTAGCGCTTTCCCTCAGAATTCAGGGAAGAGACTGTGCGCTGCTCTTCCGTTGTTGCGTGA
 GAACCGCTGCGCCCTTCCACCAATATCACCTCGCTCCATCTTTGAACTCAACACAGGGAACTAATCTCAGC
 CTGCTCCTCTCCCGAGTCCCAAGTCACTCCCTCCATCCCTCAGCTTCTCTCAGCTCTAAGGGAATATCAACTGCC
 AGCACAGGGGCCCTGAATTTATGTGGTTTATACATTTTTTAATAAGATGCATTTATGTATTTTTTAATAA
 GCTGAGGAATTAAGTTTAAAAAATAA

FIGURE 142

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCF
FDPNFKSTALVVDGELYTGTVSSSQGNDPAISRSQSLRPPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFFPNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFKDHFMDGQVR
SRMLLLQPQARYQRVAVHRVPGHHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQ
QLATRPWIQDIEGASAKDLCSSASSVSPSFVPTGEKPCQVQFQNTVNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLVLVGTQQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVPIISTSRVSAPAGGKASWGADRSYKFEFLVMCTLFVLAVLLPVFLFLYRHRNSM
KVFLKQGECASVHPKTCPPVLPETRPLNGLGFPSTPLDHRGYQSLSDSPPGARVFTSEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGGCCGGCGGCCGGCTACGAAGAGGACGGGGACAGGCCGCCGTGCGAACCCGA
 GCCAGCCAGCCGGAGGAGCGCGGCGAGGGCGGGAGCCGGAGCTCGTCTGCCGCCGCCGCTGTGTCGCCGCTCG
 TCCGCCGCCGCTCCCGCGCGGAGGAGGAGCCGCCGCTCGCGCCGAGCGCGCGTGTAGCGCGCG
 CGGGCATGGTCCCCCTTTAAAGGCGCAGGCCCGCGCGGGGGGGGGTGTGCGGAACAAGAGCGCGGGCGGGG
 CTCTCGGGCGCGCTCGGGGCGCGGATGGCGCGCGCGGCCCGCGCGCGCGCGCGCTGCTCCCGCGGGCGCTCG
 CGGCCGTAGGGCGGGCTGGCCTCGTGGCGCGGGGCGAGCGGGCTGAGGGCGCGCGGAGCTGTGCGCGGGCGGGC
 GCGCGCGCGCGCGCGCGCGGGCGGAGCGCGCGCGGCGATGCGCGCGCGCGCGCTGGCTGAGCTGCTGAGCTGC
 TGTCTGGGCTCGTCTGGGCTTGTGCTGGCTCGCGGCTCGTCTGCCCGGGCTTCCAGTGTGAAGCGAGGG
 GCCACCGCGCGCGCGCGCGCGGGGCTGCGGCTCGGGCAGCGCGGGCTTCCAGCGCGCGCGCGCGCGCG
 GCGATGCGCGCGGGCGCAGCTGTGGCGCGCGCGCTCGGACCCAGATGGCGCGCGCGCGCAGCAGAACTTTCTCT
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCGCTGGCGCGCTACGAAACATGGTCCAAGACA
 TTCTGGGAAAGTTTCAAGTTCTTCAAGTGGGGTCTGACACATCTGTACCAATTCAGTAGTGCCACTACGGG
 GTGTGGAGACTCTACCGCGCGCGAGAAAGTCTTTCATGATGCTCAAGTACATGCAACCACTACTTGGACA
 AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAGAGAGACCGTCTGGAGAATCTTCTGAGGAGTT
 TGAACAGCAGCGAGCGCTCTTTCTGGGCAGACAGGCTGGGCACACCGGAAGAAATGGGAAAATGGCCCTTG
 AGCCTGGTGAAGACTTCTGCATGGGGGGGCTGGCGTGATCATGAGCGGGAGTGCTTCCGAGAATGGTGCCG
 ACATTGGCAAGTGTCTCGGGAGATGTACACACCCATGAGGACGTGGAGTGGGAAGTGTGTCGGAGGTTTG
 CAGGGGTCCAGTGTGTCTGCTTTATGAGTCCGGCAGCTTTTTATGAGAATACGAGCAGAAACAAAGGGGT
 ACATTAGAGTCTCCATACAGCAACACAGAAATCACCAAGCTATCAATTACACCCCAAAAACCCACTTCAAGT
 ACAGGCTCCACAGCTACATGCTGAGCGCAAGATATCCGAGCTCCGCCATTCGCAACATACAGCTGCACCGCGAA
 TTGCTCTGATGAGCAATACAGCAACACAGAAATTCATAAAGAGGACTCCAGCTGGGAATCCCTCCGCTCTCA
 TGAAGTTTCAGCCCGCCAGCAGAGGAGGATTCGGAATGGGAGTTTCTGATGGAAATATCTGTATTCCGAG
 TTAGCGCGAGCCCTCGAGAGGAATGGACTCGGCCAGAGGGAAGCTTGGACGACATTTGATCATGAGCTCA
 TGGAGATGATCATGTCGACCGCCAGACAGAGGGCGCATCTTGAAGTCTTCAAGAGGTCAGTAGCGCTACGCC
 GGGTGAACCCCATGTGTGGGGCTGAGTACATCTGGACCTGTGCTTCTGTAACAAAAGCAGAAAGGGAAGAAA
 TAGCGCTCCCTGTGAGGAGGCGCGCTATTACAGCAGACTTTCAGCAAAATCAGTTTGTGGAGCATGAGAGC
 TGGATGCAACAGAGTTGGCCAGAGAATCAATCAGGAATCTGGATCTTGTCTTCTCTCAACTCTCCGAAGA
 AGCTCGGCCCTTTCAGCTCCCTGGTCCGAAGAGTGAGCACAAGAACCCAAAGATAAAAGATAAAATACATCA
 TTCTTTGTCTGGGCTTTCGACATGTTTGTGAGATTTATGGGAACCTTTGAGAAGAGCTGTCTTATCCCAATC
 AGAACGTCAAGCTCGTGGTTCTGCTTTCAATTCTGACTCCAAACCTGACAAGGCCAACAAGTGAACATGATGA
 GAGATTACCGCATTAAGTACCTAAAGCCGACATGCAGATTTTGGCTGTGTCTGGAGAGTTTTCAGAGCCCTGG
 CCTGGAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCTCTTCTCTGCGAGCTCGACCTCGTGTTTACTA
 CAGAATTCCTTCAGCGATGTCGAGCAAAACAGTTTCTGGGCGCAACAATATATTTTCAATCATCTTCGCGAGT
 ATGACCAAGATGTGTTTATGATGGGAAAGTTCCAGTGACAACCAATTTTGCCTTACTCAGAAAACTGAGCTTCA
 TCCAAGAGCTGGGGCTGGAGGATGTGGACCTTTTCAACAAGTTGTCCAGCGAGGTTTGAAGACGTTTAGGAGCC
 AGGAAGTAGGAGTAGTCCAGCTCCACCATCTGTCTTTGTGATCCCAATCTTGACCCCAACAGTACAAAGTGT
 GCTTGGGCTCCAAAGCATCGACCTATGGGTCCACCGCAGCTGGCTGAGATGGGCTGGAAAAAATGATCCAA
 GTTACAGTAAAGCGACCAATATAATGGCTCAGTGAGGACAGCCTAATGTCGAGCTTGTGCGAAAAAGACGTTT
 TATATTAATAATTTATTTTCAAAAAATTTTGTATGATCAGTTTGTGAAGTCGATACAGAGATATATTTTAC
 AAGTGCGTTTCTTACATAGGACTCCTTTAAGATTGAGCTTCTGAAACAAGAGGTGATCAGTGTGTGCTTTGAA
 CAGCATCTCTTGTCGAACATTTATGAGCAGACCTGCTTAACTTTGACTTGAAGTACCTGTGATGAACAAACTTT
 TTTAAAAAATGTTTCTTTGAGACCTTTGCTCCAGCTTATGGCAGAAAACGTGAAACATTTCTGCAAGATTA
 TATTGTGTAACAAACATCTGTAATCTGTAATGTTCTGTGTGATTTGATTTGTTTCCACAGATTTCACTTTTGT
 GTTTGTTTCTTTTCTTTTACAAATGTTTAAAGCCATTTCAATGTTCCAGTTTGAAGATTAAGAAAATGTGTAATA
 GTCTGTTTTCATGTCCTTCAGGAGAGCTTCCAGAGTTGATCAITTCCTCTCATGTTACTCTGCTCAGCATGGC
 CAGTAGGTTTGTGTTGTTTGTGTTGTTCTTTTGTGAGACGAGCTCTCACTCTGTACCCAGGCTGGAATG
 CAGTGGCGCAATCTGGCTCTGTTTAACTCCACTCCCTCGTTCAGCAATTCCTCGCTTCCGCTCCGAGT
 AGCTGGGATTCAGGCAACACACACAGCCAGNATGTTTTTTGATTTTATGATGAGACGGGCTTTCACAT
 CGAAGCCAGCTCGCGCAGCTAGGTTTAAAGCAAGGGCTGAGCAAGGCACAGTAGATGTGCGTGTCTG
 TGGTACTTTCATTCCGCTAAATAGACCTGCCATTAATTTCAAGAGGATTTGGCATTTCTCTTCTGACCCCT
 CTCTTTAAAGGTAATAATTTATGTTTGAAGTACAAAGATCAATTTACAAATAATCTGATGTACACAGCT
 GAAACATACACATACACCTTAATCAAAACCTTGGGAAAAATGTATTTGGTTTTGTTCTTCTATCGTCTG
 TTTTATCTGGTGGAGATGTTTTTCACTTCTTCAATTAAGTTTGTGTTTCTTCTTCTTGTATCTGAATACCTTAA
 TTTTATTAATATCTGTTTTCAGAGCTCTGCCATTTCTGAGTACCTGTTAGTTAGTATTTATTTATGTTGATCGG
 GAGTGTGTTTGTGTTTATTGTCAGTAAACGATCTCCAAGATTTCCCTTTTGAAGAACGTTTTTCCCTTC

10017407.12301

FIGURE 143B

TTAATTTTATATTCCTTACTGTTTACTAAATATTAAGTGTTCTTTGACAATTTGGTGCTCATGTGTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAACAGTGATAGACTTGCCATTTTAATACAGTCAATGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTTGGAAAAATAACCAAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAACTTAACACGAAAAA

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FIGURE 144

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
>subunit 1 of 1, 802 aa, 1 stop
>MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGRDRNFLFVGVMTAQKYLQTRAVAAAYRTWSKTI PGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRIENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWVSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQREE
ILEWEFLT GKLYLSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNP MYGAEYILDLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVFPQLPGSKSEHKPEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEF SRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGDIVRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
 TTTCGGCCTTGAGGTTCCACGCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCCTATGAAGCCCTTAGTCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
 CAAGTTTTAGAGAACCTAGTACGAAGTGTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
 TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
 ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
 ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCTCAGCTCT
 CAGGTGAACTGCGATAGAAAAACCCGAAGAGTTTGAAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTCTTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC
 TAGATCTAAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCAATACATTAATAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTTATTAAACAATAATATAAAATTTTAAACCTACTTGATATTCATAACAAAGCTGA
 TTTAAGCAAACTGCATTTTTTACAGGAGAAATAATCATATTCGTAATTTCAAAGTGTGAT
 AAAAAATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA
 ATTTTCATATGCACTAAAAACCTAATTTAAAAATAAAATTTTGTTTCAGGAAAAA

FIGURE 146

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTPTGGFTPEIGKKKHTESTPFWSI
KFNNVSIVLHAEEPYIENEEPEPEPEPAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSALAAAAEHKLKTMYSQLLPVGRTSNKIDDIE TVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCTGCGCCTGAGACAGCTGGCCTG
 ACCTCCAATCATCCATCCACCCCTGCTGTCACTCTGTTTTCATAGTGTGAGATCAACCCACA
 GGAATATCC**ATGG**CTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTCAAGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGAGGACCGCGTGTCT
 CCTGCTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGGCGGTTCTTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGAGAACTGAGTTTGTGAAGGACTCCATTGTCAGGGGGGCGTGTCTCTCAAGGC
 TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCACTTCCAGATTTTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCCTCTCATTTCCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTTCCCCCAGC
 CCACAGCCAAAGTGAAGGTTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTGTGTTCCATCCACCTTGTCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTCTATGGGGATGATAATTGTTTTCTTCAAATCCAAGGGGAAAATCCA
 GGCGGAACCTGGACTGGAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCGGAAACAG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTG
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTTCAC
 ATTCAATCCCCATTTTATCAGCCTCCCCCAGCACCCCTCTTACACGAGTAGGGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTATACC
 CTGCTGACATGTCAGTTTGAAGGCTTGTGAGACCCATATATCCAGCATGCGATGTATGACGA
 GGAAAAGGGGACTCCCATATTTATATGTCCAGTGTCTTGGGGAT**CGA**CACAGAGAAGACCCCTG
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGC
 CCCAGCTTCTCTCCGGAGCTGCGCACAGAGAGTCAAGCCCCCATCTCCTTTAGGGAGC
 TGAGGTCTTCTGCCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGAT
 TGGCCTGACCCCTGTGGGAGTCAGAAGCCATGGCTGCCCCTGAAGTGGGGACGGAATAGACTCA
 CATTAGGTTTGTGTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
 CAGGCTCCTCATTTGTCTAGTCACGGACAGTGATTCTTGCCCTCACAGGTGAAGATTAAAGAGA
 CAACGAATGTGAATCATGCTTGCAGGTTTGAGGGCACAGTGTGTTGCTAATGATGTGTTTTTA
 TATTATACATTTTCCCAACATAAACTCTGTTTGGCTATTCCACATTAATTACTTTTCTCTA
 TACCAATACCCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG
 GAGGTAGGATTTTCACTGATTCTATAAGCCACGATTACTGATACCAAAACCAGGCAAG
 AAAACAGAAGAAGAGGAAGGAAACTACAGGTCCATATCCCTCATTAAACACAGACACAAAAA
 TTCTAAATAAAATTTTAAACAAATTAACATAACAAATATATTTAAAGATGATATATACTACT
 CAGTGTGTTTGTCCCAAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAGGTGAATT
 CAGCACATTAATAAGTAAAAAGAAAAACATAAAAAAAAAAAAAA

FIGURE 148

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETTFQPPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDVRGKNNVTLS
PNNGYVWLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVS
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAGAGTTTGTGGGAACCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAGAAGACCTACAA
 TTACTATAGCACATTGTCAATTACAAGTACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAATGCATTTTATAAA
 TCTCCATTAAAGGAAGAATTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTGTAGATTCTACTGAGGATCCTGAAACTGTAG
 ATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCATAAGTA
 GATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACCGAAGAAGTAAAACCTTAGGTGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTGTGAGTGCTGCTCACTGTTTTACAACATATAA
 GAACCTTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGAAGTCTGGAGGACCACTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAAACAG
 CCTGGTGTATATCTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGAC
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCTC
 AGCTCCTCTCATTTGACGAAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA
 TAAGAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTCTTAGT
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC
 ACTTCATCATTTTAGGAAGTATGGGAACAAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTCATTTCCAAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAACTTCATGCAATGTACTGTGTTCTAAGCAAATTAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVYPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTGAGCTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
 CGTGACCTTCTTGGTTCACAGAGCTCAGCCCTTGGCCCTCAAGACTTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCTTTGCCGGCTGTCCCTGCGACTACGACCACTGC
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCTGCCTGTGCCC
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGTCTCCACTACTGG
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCGCTGAACGCTACGGTCCG
 CAGAGCCGAACCTGAAGGGGCTGAAGCCAGGGGGCATTATGTCGTTTGCCTAGTGGCCGCTA
 ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
 CCTGCCTTCGGGCCTTGACGCCGCTTGCGGTGCCGCCCAACCCCGCACTCTGGTCCACGC
 GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGCATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGAGGGGCGCTC**TGA**
 AAGGGCCTGGGGCATCTCGGGCACAGACAGCCCACTGGGGCGCTCAGCCTGGCCCCCG
 GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGCTGGACGCGAGCTGGGAGCCAGCCCCAG
 GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAAAGTCCGGTACTT
 GGCGCTTTGTTTCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTAA
 AGCGGCCAGATAATAAATAATGTAACCTTTCGGTTAAAAAAAAAAAAAAAAAAAA

FIGURE 152

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRVQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLDRWGCPRRAARAAGAL

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCCGATGAGCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCCGG
 CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAGGATGGGGC
 TTCTCCCTTACGGGGCTCACA**ATG**CCAGAGAAGATTCGTGAAGTGTCTGGCCTGCCTGCT
 CTACGCCCTCAATCTGCTCTTTTGGTTAAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGA
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGGTAGAGGAAGCAGTC
 ATTTTGACTTACTTTCTGTGTGTTTATCCGGTCATGATTGCTGTTTGTGTTCTCTTATCAT
 TGTGGGATGTTAGGATATTGTGGAACGGTGAAGAAATCTGTTGCTTCTTGCATGGTACT
 TTGGAAGTTTGCCTTGTCAATTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG
 GAACCTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAACT
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCAGAT
 TCCTGCTGTGTTAGAGAATTTCCAGGATGTTCCAAACAGGCCCCACAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGTGGGAAGAAATGTATTCCTTTTTCAGAGGAACCAACCACTGC
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGAGCCTGGGACAGACCAATGATGTC
 CTTGAAGAATGACAACTCTCAGCACCTGTATGCTCCCTCAGTAGAACTGTTGAACCAAGCC
 TGTCAAGAAATCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTA**TAA**AAAGAAATGTACAGAAGAAACCAACAACTGTTTTATTGGACTTGTGAATT
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAATGTTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAAGTTTCATGTATAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTT
 CGCATCCATGCAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTACTTT
 CTACCAACTAGTATATAAGTACTAATTAATGCTAACATAGGAAGTTAGAAATATACTAATA
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATATATATCAGAAAACCTTC
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAATATTCTTACCACTTAAAA
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGATATATAAGTCTGTGTTAAA
 TCTGTATAATTAGTCGATTTTCACTTCTGATAATGTTAAGAATAACCATTATGAAAGGAAA
 ATTTGTCCTGTATAGCATCATTATTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT
 CCTGGGCTTATATTACATATAACTGTTATTAAATACTTAACCACTAATTTTGAATAATA
 CCAGTGTGATACATAGGAATCATTATTCAGAAATGTAGTCTGGCTTTTAGGAAGTATTAATAA
 GAAAATTTGCACATAACTTAGTTGATTGAGAAAGGACTTGTATGCTGTTTTCTCCCAATG
 AAGACTCTTTTTCAGACTTAAACATTTTTTAAAGGCTTATCTTTGCCCTTCTCCAAACAGAA
 GCAATAGTCTCAAGTCAATATAAATTTCTACAGAAATAGTGTTTTCTTCTCCAGAAAAAT
 GCTTGTGAGAATCATTTAAACATGTGACAATTTAGAGATTCTTTGTTTTATTTCACGTGATTA
 ATATACTGTGGCAAATACACAGATTATTAATTTTTTACAAGAGTATAGTATATTTATTT
 GAAATGGGAAAGTGCATTTTACTGTATTTTGTGATTTTGTGTTTTATTCTCAGAAATGGA
 AGAAATTAATGTTGTCATAATATTTTCTAGAGAGTAA

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC
 TGCACCTCGGGCCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGGTTGTCTCATCAAGG
 TGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCAGAGGCCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCCACTGCAGGTGCTGG
 ACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA
 TGTGTTTGAATCACAGAAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTC
 TCTCAGGCTCCCTGGTCTCCTGCACTGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCCGT
 GTGGTGGGTGGGGAGGAGCCTCTGTGGATTCTTGCCCTGGCAGGTGAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACT
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAA
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
 GGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCAACGAGAAGA
 TGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGCTGACAGTGGTGGGCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCCGAGCACCCCAAGGATATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTTGCACTGCTGGGAGCCGCTTCCCTCTG
 CCCTGCCACCTGGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCC
 CTCCTGCCACAGCCTCAGCATTCTTGGAGCAGCAAAGGCCCTCAATTCTGTAAAGAGACCC
 TCGCAGCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
 AGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACCTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAGCCAGCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA
 CTAGAGCAAGAAACAGTGTGAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT
 ACCTACTGTTGTCTATTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAAAA

FIGURE 156

```
></usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVVKPLRKFPRIMETFRKVGIPIIIIALLSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAEATACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGGEEASVDSWPQWQSVISQYDKQHVCGGSILDPHWVLTAACHFRKHTDV
FNNKVRATSDKLKGSFPLSAVAKIIIEIFENPMYPKNDIATMLKQDFPLTFSGTVTRPICLPFED
ELTPFPALDWIIIGWFTKQNGGKMSIDLLQASVQYIDSTRCNADDAYQGEVTEKMMCAPIGE
GGVPTCOGSDSGGELPYKQSDOWHVVGI VSWGVGCGGSPSTPGVYTKVSAYNLWIIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

TGTGGCATTCTCAGAGGGAGGGAACGCGAGCGGCATCCCCAGGCTCCAG
 CATGCGCCCTCCACGCCCTGGCGCTTGACCCTGGAGCCTCTGGCGC
 TGTCTGCGACGACGACCGGGGGGAGGCGGGCAGGGGCCCATGCCA
 TAGGGCAGCTTAGCTTTCTTCCACAGAGAGGCCCTCAGGATTTGACA
 TCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGG
 TGATACCGTGGCGCAGCCAGCAGAAAAAAGAGATGAATGTGCCTTTA
 TCAACTTTCATCCGTGCTGTGGTTCTTACAATTGTCACCCATCTCTACA
 TTTGTAGCTTCTTATTGAACCTCAAGATTCTACTCTGTGGCCATCTCGG
 AAAGCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG
 ACTTCTCGGGCAGTGAGCCCATCTGTATGCGCAGCATGGGATCCGAGC
 CTGGGTGCATCATACGCCCTCTTTTGGCGAGCCATCCCTTCGACCC
 CAGCCAGCGAGTTTGAATCTTCTTGAGAGCTCCACACTCGCGGGTCC
 CGAAGAAAGTCTCTCGAGAAGGTGGACCACTTCTCTGAAGCCCGAGC
 CTTTCAACGTATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCA
 TCTCCGAGTGGCAGTGTGGCGGGACAGGAGATCTCGGTTTGTGCTCT
 TTTAAGGGGAATACAGAAGTTGAACAAGAAATCTACGCTTGACTATA
 GGCCAGCGAGCTTGTCTCAGTGGGCCCTCTCTGATAGAGCCTGACCT
 AGCAAGTGGTGGGGAGGCCCTGCTGGTGAATCTGGGCTGGAGTATA
 GCGCTTGATGGGCACAGCCATCTGTGATCTAGCTGGGAACCAACACAG
 GCGCCATGAGCAGCTGCTCATCTGGTGGAGAGATTCAGTCTTCCCTGACC
 CCCCCACCGAGGTCAGTGTCTTGAGGCTTCTCAGGAGGTTGTGGA
 ATGAGAGCTGTGTGGAGCTGTGCTCTTGCCGGGAGCCCCACTGTGCTC
 TCTGTGAGCTCCCCATGCCCCACTGTGAGCTTGGCCTTCTATTATT
 AAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGG
 GGGCAACTGAGAAATGGCTTTTATACCTGTGATCTCTACTGGGTGG
 TCTCTGAACTGCGCAGGCATCCCCGGGAGCATGTGAAGTCCCGCTGTG
 ATGCCAGCAGTCTTACTGCGCCCACTTGACTACTGCACTGTCTTACT
 TCATCTCTGTGGCCTTCCCAATTGAGAGCACTCGGGGCTCGGGGCAAGG
 GGGAGAAGGCCCTTTAAGCAGAGAGCAACACCTTCAGTCTCCCAAGG
 CAGCTGACACAACTGCTTAGCAGCTAGGTAGCTTAACTCTAGGCA
 GGGCATCTGGCTGGCGGGCCCAAGCACAGGCTGACTAGGATGACAG
 GAGAGAGAGCTTCTGCTACTCTGCATCATGTAGACATCAGAGGGTG
 GACTCCCTTCTACCAAGCATGAGCTCTCTAACAGGGTGGGGGCTAC
 AGAAGAACCTGGAGAGGATCTCTCAGTTCTGGCCATTTCAGGAGAACCT
 TAAAAAACCTGGCTGCTCCAGGACCTATGTGTAATGAACACCAAACTC
 CTGGAATCTCCACTGTAGAGCTGGCGTTTGAACACCAACACTCTCT
 CCTCTCTGCTTCCCTTACGAGCTGTGACCGCTGACTCCCGAGGAATC
 TGTGCTCAGTTGGGGCAGACTCTGATCCCTCTGCGCCTTGGCGAATGG
 TTTTACCCTAGCTGACCCCTTCACTCTCCGCCCTCCCTTTGCTTTGT
 GAGCTCTTATTATTTTTAAAAAATAAAGCTTTAAAAAA

FIGURE 158

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGPMRVRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGSGDNTLYVGAREAILALDIQDPGVPRLLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDDPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDSFVAAIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVVGEEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLLHKAUVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFAVLVSGALIIIVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVEDADNNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGCGCGCAGGGCGCGCAGCCAGGCTAGATCCGCGGCTTCGGTAGAAG
 TGACGATGGCTGCCAGCGAGTGCCTCTCTTCTAGTGGGCTCTCTTCCCTGGGGTCCGCTGC
 TCAGAGGCTGCCAAAATCTGTACAATATCTACAGTAGGTTGGAAGCCATTATCTACTGATGGA
 CCGGGTTTTCTCAGATTCTTCAAGATCAGCGTCAATATGTCACCATGCTTAACCCACAAAGAC
 GTCCTTTTATGCGCAGATTTTAAAAGGAAGAAAATCATATCAAGTTATCACTTGGCTTGCAC
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGATTTGATTTCTTCTGGAAGAAACTTAGG
 TGGCAGAGAGAAAATTTGAAACTATTATAATGTCTTAGAATACCTTGGCGTTGCAGTGCAGT
 ATTTTTTTAAATGAAAGAGATATCATGGATTCTTTAAGAATGAGAATCTGCATGGTGATA
 GTTGAACCTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC
 CATCTCTTTCACCTTCATTCCGGCTCTTTTGGAAATTTGGGGTACCAATCCCGTTCTCTATGTT
 CAGTATTCGGTTCCTGCTGACTGATCAGATGGACTCTGGGGCCGAGTGAAGAAATTTCTTG
 ATGTTCTTTAGTTTCTCGCAGGAGCAACAGCACATGCAGTCTACATTTGACAACACCATTCAA
 GGAACATTTTACAGAGAGGCTTAGGCCAGTTTGTCTCATCTTCTACTGAAACGAGAGTTGT
 GGTTCATTTAACTCTGACTTTCCTTGGCTTTGATTTTGTCTGACCTCTGCTTCCAACTGTTTAT
 GTGGGAGGCTTGATGAGAAAACCTATTAAACACGATACACAAGAGCTGGAGAACCTTCATTGC
 CAAGTTTGGGGACTCTGGTTTGTCTCTGTGACCTTGGGCTCCATGTTGAACACCTGTGCGAGA
 ATCCGGAATCTTCAAGGAGATGAACAATGCCTTTTGCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCCAGTGTCTCATCTGGCCCAAGATGTCCCACTGGCTGCAAAATGTGAAATTTGGGA
 CTGGCTTCTCAGTGCAGTGCCTCTGCTGATCCCAAGCATCGCTGTTGTGTCACCCACGGCG
 GGCAGATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGGATCCCTCTCTTT
 GGAGAACCGCTGAAACACATGGTCCGAGTAGAAGCCAAAAGTTTGGTGTCTTATTCAGTT
 AAGAAGCTCAAGCGAGAGACATGGCTTCTAAGATGAAACAATCATGGAAGACAAGAGAT
 ACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCTGCGCTCCACCCGCTCAGCCCCACACAG
 CCGCTGGTGGGCTGGATTGACCACGTCTCCAGCAGGGGGCGCAGCGCATCTCAAGCCCTA
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTGTGTTTCTGCTGGGG
 TCACTCTGGGGACTCTATGGCTTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCGAGAAAGTGAAGGACACATAAGAGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
 GCGATGTCACCATTCTTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCTCTC
 TATTTATCTCTCTGTTTCTTGAAGACAGGAAAAATGGCCAAAACATCTTCTTCACTTGC
 TAATTTTGGTCAAAATTCATCTCTTACTAGCTCTGCTGGCTGCTAGAGAATCTTTCAGCTCT
 CTTGTCTCTCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTT
 GACCACATGACCCTCAGATTTCAGCCTTAAAAACCACTCTCTCTCATGCGCTCTCCGAA
 TCACACCCTGACCTTCTCCAGCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCTCGCCC
 TACTATCTATATGTGAATAAATCAAGAAAGAACCTTGCCATATTTCTTAGTTTCTGTTT
 TGTTCTCCCACTATTCTCTTCAATGCTCAGGAGCCTGCACTGTGTGTTGAGATTGAGGCG
 CGGACACAGGCTCAGAGTCTCCACATTGGGTCCCTGTCTGTGGTGGCCACAGTGAGCTCCT
 TCTTGGCTGAGCAGGATGGAGACTGATAGTTTCCAGATTCTCTGAAAAATAAAGTTTACA
 CGGTTATCTCTCCCCAACCTCACTAA

FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGGKPFVAILSTSFGSLEFGLPIPLSYVPV
FRSLTLDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAEWLF
INSDFAFDFAFRLLPNTVYVGGLMKPKVPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPWHEQYLFDFVFVFLGLT
LGTWLWLCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGCGTGTGATTGTGGGGGATTTGAAGAGAGGAGGAATAGGAGGAAGGGGTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTCACACCCGTCACACACATACCATGTT
 CTCCATCCCCCAGGTCAGGCCCTCAGTGTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCAAAGCCCA
 ACTGCTGCTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTACGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA
 AGACCGGGGCACTTGTGGGTGACAGGCCCTCAGCCATGTTGGGAGCCAGGCCACTGGC
 TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC
 GGGTGGGCCCAGGAGGGGTGAGAGCCCGTCTGCTGGAGGGGGAGTGCCCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGGCCGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
 GAGTGGCATTGTGCGGTCCGAAGCCACCACATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACAGGTCTCGGTGAACGAGGGCGGTGGCTTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCCCTGTCCGGGGTGCTACAGCTTCCGGTTCCATGTGGTGAAGG
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTATCTCAGCC
 TTTGCCAATGATCCTGACGTGACCGGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGA
 CCTGGGGACCGAGTGCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAATACT
 CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCTGAGGAGCCCAAGTCTTTCAAGCACAGAAT
 CCAGCCCCTGACAACCTTTCTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCCAAGTTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCCACCCACCCACCCCAAGTTTAA
 CTCCCAGCCACCTGTGCATCTGTTCTCTGCCAGCCTAGGATCAGGGCAAGGTTTGGA
 AGAAGGAAGATCTGCACTACTTTGCGGCCCTGCTCCTCCGGTCCCCCAGCCAGCTTCCT
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGGCCAG
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCCTGTGAGGAAAGCCAGCATCAGGATC
 TCAGCCAGCACCGTCAAGAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGTGATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCCCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTTGTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCATGCATCCTCTGCTTGGCCACCTCCTGAAACTGCTCCAC
 CTTTGAAGTTTGAACCTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCTCCTCCAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCCTGAT
 CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCCTATTACCTGGGATTCCATGATTCACTCCTT
 CAGACCTCTCCTGCCAGTATGCTAAACCTCCTCTCTCTTTCTATCCCGCTGTCCCAT
 GGCCAGCCTGGATGAATCTATCAATAAAACAACATAGAGAAATGGTGGTCAGTGAGACACTAT
 AGAATTAATAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTTACAGGTACAAGTAGGTA
 GTTTCGAGAGGAAAATAAATATCAAACCTGTATACATAAAATAAAA

FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEFVLLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGLIFPL
```

Signal peptide:

amino acids 1-32

[illegible]

FIGURE 164

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVDWNTPKKGRRS
QWVRNWAUVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLRREYLMGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPTIPKLEHPTQQDIDLYHTMYEALVKLFDK
HKTKFGLPETEVLEVN

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

GGGCGGCGGGATGGGGGCCGGGGCGGGCGCCGCACTCGCTGAGGCCCGGACGCGAGGGCGGGCGGGCCCA
 GGGCCGAGGAGCGCGCGGCCGAGAGCGGGGCCGCGAGGCGAGCCGGGGACGCCCGCGGACGAGCAGGTGGCG
 GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGCGAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGA
 CGGCTGTCTCAGCGAGGGGGCGGTGCACCCGCTCCTGAGCAGCGCATGGGCTCTGCTGGCTTCTTGAGACCCA
 GTTCGTGCTGCACTGCTGGTGGCTTGTCTTCGTGGTGAGTGGTCTGGTCATCAACTTCGTCCAGCTGTGCAC
 GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCGCCTCAACTGCGCCTCGCTACTACTCTGGAGCCA
 ACTGGTCATGCTGCTGGAGTGGTGGTCTGCACGGAGTGACACTGTTACAGCAGCCAGGCCACGGTAGAGCGCTT
 TGGGAAGGAGCAGCAGTCATCATCTTCAACCACAACCTTCGAGATCGACTTCTCTGTGGTGGACCATGTGTGA
 GCGCTTCGGAGTGTGGGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGGCTGGAC
 GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTCAAGAGCGCTGAG
 GCGCTGTCCGAGTACCCCGAGTACATGTGGTTCTCTGTACTGCGAGGGGACGCGCTTCACGGAGACCAAGCA
 CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGCTTCTCTGTCTCAAGTACCACCTGCTGCCCGGACCAAGGG
 CTTCAACCACCGAGCTCAAGTGCTTCGGGGGACAGTCGAGCTGTCTATGATGTAAACCTGAACTTCAGAGGAAA
 CAAGAACCCTGCTCTGCTGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCTCT
 GGAAGACATCCGCTGGATGAAAAGGAGCAGCTCAGTGGCTTCAATAACTGTACCAGAGAAGGACGCGCTCCA
 GGAGATATATAATCAGAAGGGCATGTTCAGGGGAGCAGTTAAGCCTGCCCGGAGGCCGTGGACCTCTCTGAA
 CTTCCGTCTCTGGGCGACCATTTCTCTGTCTCCCCCTCTCAGTTTTGTCTGGGCGCTTTGCCAGCGGATCACC
 TCTCCTGATCTGACTTTCTGGGGTTGTGGGAGCAGCTTCTTTGGAGTTCGACAGCTGATAGGAGAAATCGCT
 TGAACCTGGGAGGTGGAGATTGCACTGAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
 CAGTCTCAAAAAAAAAAAAAACAAAAAACCCAGAAATTCGGAGTTGAACCTGTGTAGTTACTGACATGAAAA
 ATTCATAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
 TTTCAAGCTAATGAAAAAGAAATGAAGAAAAATTAACAGCCTCAGAGACCCTGGTGACCGTCACACAAATCAA
 CATATGCATGATGAGATCCGAAAGGAGAGGAGAGAAAGGCTCAGAAAGAAATGGCCACAGCTGATGAAAAACA
 GTAACCTACCCACTCAGGAAGCTCAGTGAATCCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCA
 ATCAAAAGTGCAAAATCAAAAGAAATCTTGAAGCAGCAAGAGATGAGCAACTTATCTTGTCAAAGGATCTTGG
 ATCAGATTAACAGCTCATTTCTCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGCCAA
 AACCTTCAACTGTAAATATTGGACCTTTGAGTCTTAGATGGCTCTGACCTTGTCTTTCAGGGACAGATTTTCA
 ATTTAATCCCTAATAACAMTTAGTCAAGCTTCTTGTACCTGTAGGAAGGCTGTCTTTAGGCGGGCAGAGTGGC
 TTACACCTGTAAATCCAGACACTTTGGGAGGCCAGAGCGGTGGATCATTTGGGGTCAAGCTGATCTCAAACTCCT
 GAGTTCAGGTGATCTGCCCGCTCAGCCTCCCAAAGTGTGTGATTGACAGGCGTGAGCCACTGCGCTGGCCGGA
 ATTTCTTTTAAAGCTGAATGATGGGGGCCAGGCACGATGGCTCAGCGCTGATCCCAAGTGAATCTTGATTGTA
 AACATGCACCACCATGCCTGGCTAATTTTTGTATTTTTTAGTAGAGCTGTTAGCCAGGCTGGTCTCGATCTCCT
 GACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCTGGCCTTGA
 GCATCTTGTGATGTGCTATTGGCCATTGTATATCTTCTATCTTCTTGGGGAAATGTCTGTTCAGATCCTTTG
 CCTTTTAAATTTTTATTATTTATTTATTTATTTTGTAGACAGGCTCTTGTCTGTTGCCAGGCTGGAGTA
 ATTTCTTGCACAGTCTTGGCTCAGTCAGCCTCGACCTCCTGGCTGACGATGATCTCCCACTCAGCTCCCTTGT
 AGCTGTATTTTTTTGTATTTTTGTATTTGTAGCTGTAGTTTTGTATTTTTGTGGAGACAGCATTTACCATGA
 TGCCAGGCTGGTCTGAACTCCTGAGCTCAAGTGATCTGCTGCTTCAAGCTCCCAAAGTGTGGGATTACAGA
 CATGAGCCACTGCACCTGGCAACTCCCAAATTAACACACACACAAAAAACCACTGATTCAAATGGGCA
 GAGGGCGGGGTGTGGCTGGCACTACAGGGAGATGAAGTGGGAGATCGCTTGGGCATGAGAAGTCGAGGCTG
 CAGTGAGTCAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCTGTCTC

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVSVSGLVINQVQLCTLALWPVSKQLYRRLNCR LAYSLWSQLV
MLLEWWSCTECTLFDTQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFVGLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTINFRGNKNPSLLGILYGGK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFGVAASFVRRLLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTTAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
 GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGTTGGTGGCAGGCAGGCCG
 GCTTACGCCTGATACGGCCCTGGGTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
 GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCCTGGGATCTGCCTATACCTTCTT
 TTCTCTAACCTGGCATAACCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGT
 ACATGTGGTGTTCTCTTGTCGTTCTCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCT
 TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCATACTCTTCCTACTTAATATGTAGTC
 ATCCTGCAAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTGTGTTAATGCTCTCATAAGACCACTTGTTTCCCTTTTGACGCACTTGCCACTCAGTTGTA
 TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
 TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCTACATGTGGTGGGTGCT
 CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
 GATGGTGTAGGGCCAGCATTGTAAATTCACAGTTGACTGTGCTTGTGAATTATCTGGGGA
 TGCAGTCTCTGATTCACTAGGCCAGGTTGGGCATCTCTAACAAACTCCACGTGATGCTGA
 TGCTGGTCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
 TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCAACATGGTGGAACCCCATCTGTACTAAAAATACACAAATAGCTG
 GGCATGGTGGCACATGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAA

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHS LQCPGAATRH IHL CVCF SFALALGH FLLISLVGKGLSLSCGVGGRQAGLRRLIRPWVRR
EGKINFYTN GDSWGLRPASSVKFLGSAYTFFSLTWH TLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:**Signal peptide:**

amino acids 1-28

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FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
 ATTAATACTGTTTTTTGTCTCTTGTAAGTACGCTTTACCTTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCAAACCTGACCTTCACTCTGGAACGAGAAGAGGTTTCTACCCAC
 ACCGTCCCTCGAAGCGGGGACAGCCTCACCTTGTCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCAGCTCTGGAGGCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGGTA
 GCTGCGGCTTTCAAGGTGGGCTTGGCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATT
 CATAGGCGATGGCTCCCACTGCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCCTGGGG
 CCAGGACGGGCGCTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT
 CTAACCTTTTCATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
 AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCATTCTCTGGAACATGAGGGAACGCCGAGGAAAGCAAAGTGGCA
 GGAAGGAACTTGTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGC
 ATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCGCCCCGATCCAGTACCAGGTGCTG
 AAGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCATACCAG
 CCAGGGGCGCCGCTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCTCCTTCCCTC
 TGAGAGGCCCTCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
 GCTCAGTGTGTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
 AACACGGAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAGGACTGTGTGGCT
 CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTGAAATTTGAAACCCCAA
 TCCAAACCTAAGAACCAGGTGCATTAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
 CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGAGTTCAAGACCAGCCTG
 GCCACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCCTGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAAATAAAAAAGAATTATGGTTATTTGTAA

FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

Signal peptide:

amino acids 1-15

172/249

FIGURE 171

FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAFAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSRLRLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

CCGCGCCGCGCAGCCGTACCGCCCGCTGCAGCCGCTTTCGCGCGCCTGGGCCCTCTCGCCGCTCA
CGATGCGCCACACGCCCTTCAAGCCCGGGGACTTGGTGTTTCGCTAAAGATGAAGGGCTACCCCTCAC
TGCCCTTCGCGAGGATCGACGACATCGCGGATGAGCGCGCTGAAGCCCCACCCACAAGATGCC
CATCTTTTTTCTTTTGGCACACAGCAAAACGCCCTCTCGGACCCAAAGACCTTGTCCCTACG
ACAAATGTAAAGACAAGTACGGGAAGCCCAACAGAGGAAAGGCTTCAATGAAGGGCTGTGG
GAGATCCAGAAACACCCCAACGCCAGCTACAGCGCCCTCCGCGAGTGAGCTCTCCGACAG
CGAGGCCCCCGAGGCTAACCCCGCCAGCGGACAGTGCAGCTGACGAGCAGCTGAGGACCGGG
GGGTATGCGCGTTCACAGCGGTAAACGCCACAGTGCACGACAGATGAGAGCGCACTCA
ACTCAGACAAGAGTAGCGACAACAGTGGCTGAAGAGGAAGACGCTTCGCTAAAGATGTC
GGTCTCGAAACGAGCCGAGGAAGGCTTCGAGCGCACTGGATCAGGCCAGCGTGTCCCCATCCG
AAGAGGAGAACTCGGAAGAGCTCATCTGATTCGGAAGAACACGACGACCAAGCACTTCAACCT
GAGAAGAAAGCAGCGGCTCGGCGGCCACGAGGGGGCCCTCTGGGGGGACGGAAAAAAAGAA
GGCGCGCTGAGCCTCCGACTCCGACTCCAAGCCGATTCGACGGGGCCAAAGCTGAGCGG
TGGCCATGGCGCGGTTCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCGACTCCGATGTG
TCTGTGAAGAAGCTTCGAGGGGCGAGGAAGCCAGCGGAGAAGCTCTCCCGAAGCCGCGAGG
CGGAAACCGAAGCCTCAACGGCCTTCGCTCGAGTCCAGCAGTGACAGTGACAGTACAGCCGAGG
TGGACCGCATCAGTGAGTGGAAAGCGCGCGGACGAGCGCGGAGCGCGAGCTGGAGGCCCGG
CGCGCGCGGAGAGCAGGAGGAGGAGGAGCTGGCGGGCGCTCGCGGGAGCGGAGCGGAGAGAAGGA
CGGAGGCGCGAGCGGGCGGACCGCGGGGAGGCTGAGCGGGGACGAGGCGAGGACGCGGGG
ACGAGCTCAGGAGGACGATGACGCCCTCAAGAAACGGGGACGCAAGGGCCGGGGCCGGGGT
CCCGCTCTCTCTTCTAGCTCCGAGCCCGAGCGCGAGCTGGAGAGAGGCCAAGAACTACG
GAAGAAGCCGAGTCTCTAAGCACAGAGCCCGCCAGGAAACCTGGCCAGGAAGGAGAAGAGAG
TGGCGGCCGAGGAGGAACAACAGCAAGCCCTGAAGGCTGAGCGGAGCCGGAAGCCGAGGCTCC
GAGGGCTTCTCATGAGCAAGGAAGTAGAGAAGAAAGAGCCCTCGTGGAGGAGAGCT
GCAGAAGCTGCACAGTGAATCAAGTTTGCCTTAAAGTTCAGACAGCCCGACGTGAAGAGGT
GCTTGAATGCCCTAGAGGAGCTGGGAACCTCGAGGTGACCTTCAGATCTCTCAGAAGAAC
ACAGCACTGTGGTGGCACTTGAAGAAGATTTCGCCCTTACAAAGCGAACAGGAGCTAATGGA
GAAGGCGAGCAAGATCTATACC CGGCTCAAGTCGCGGGTCTGCTGCCCCAAAGATCGAGGCGG
TGCAAGAAGTGAACAAGGCTGGGATGGAGAAGGAAGGACGCCAGGAGAAGCTGGCCGGGAG
GAGCTTGGCCGGGGAGGAGGCCCCCGCAGGAGAAGCGGAGGACAAGCCAGCACCGGATCTCTC
AGCCCCAGTGAATGGCGAGGCCACATCAGAGAAGGGGAGAGCGCAGGAGGACAAGGAGCAGC
AGGAGGGTTCGGAACTCGAGAGGAGGGGCCAAGGTTGGCTCTCTGAAAGACTGCACAGCACG
GTACGGGAGGGTCCCGACCTGGAACGGCTTGGAGGCGGCGGACGAGGACGAGGAGGACG
GGGGGCTCGGAGGCCCTGGACAGGAGAGCTGAGGACCGCGGCGAGCCAGGCCAGCCCCCG
CCGAGCTCAGGCTGCCCTCTCTCTCCCCGGCTCGCAGGAGAGCAGAGCAGAGAAGCTGTGGG
GAACCGTGTGCTGTTGTTATTTGTTTCCCTTGGGTTTTTTTTCTTCTGCTAATTTCTGTGATT
TCCAACCAACTGAAATGACTATAACAGGTTTTTTAATGA

FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYKGPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDGRG
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSQDQFTPEKKA AVRAPRRGPLGGRKKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVKKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAQKPVKVERTKRSEGFMSDRKVEKKKEPSVEEKLQKLHSEIKFALKVDS PDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEKLAGELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDEKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLD RPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCCTCGGATCTTACACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATAATTA
 ACACCATTTGAAAGAGACATTTGTTTTCATCAGTAATGCTAATAAAGATGAAAGACTTAAGGCCAGAGGCCAAGA
 TTTTACCTTTTTCTCGCTTTGATGATGCTAAGCATGACCATGTTTCTTCAGCTCACTGGCACTTTGAGACA
 AATATTTCAAGACTCAAGCTAACCTACAAAGATTTGCTGCTTCAAAATAGCTGTATTCCTTTTTTGGGTTTCATC
 AGAAGGACTGGAATTTTCAAACTCTTCTCTTAGATGAGGAAGAGGCAGGCTGCTTTGGGAGCCAAAGACCATC
 CTTTCTACTCAGTCTGGTTGACTTAACAAAAAATTTAAGAAGATTTATTTGGCTGCTGCAAAAGGAACGGGTGGA
 GGATATTATTAATTAGCTGGGAAAGTGCCTAATCAGAATGTGCAAAATTTCACTCAGAGTACTTCAGCCCTATAACAA
 AACTCACATATATGTGTGGAACTGGAGCATTTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
 GGATATTATTAATTCAAACTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGCTCTTCGATCCTCAGCAGCC
 TTTTGCTTCAGTAAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCGATTTCCCTTGGCAAGATACTGCAATT
 CACTCGATCCCTTGGGCTACTCATGACCACCACTACATCAGAAGTACGATTTAGAGCACTACTGGCTCAATGG
 AGCAAAATTTATTTGGAATTTCTTCATACAGACACCTACAATCCAGATGATGATAAAATATATTTCTCTTTTCG
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTTGAAGAGTTTGTAAAGATGATGT
 AGGAGGACAACGAGCCTGATAAACAAAGTGGACGACTTTCTTAAGGCCAGACTGATTTGCTCAATTTCTTGGAA
 TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATTTATTTTACTCCCAACAGAGATGAAGAAATCTGT
 AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAGGCTCTGCTGTTTGTGTATAGCATGGCTGACAT
 CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCTGGTGGTGAGTATGATGGGAGAA
 TCCTTATCCACGGCTGCTGATCATGTCCCAAGCAAAACCTATGACCCACTGATTAAGCTCCACCAGGATTTTCCAGA
 TGATGTCACTACTTTCATAAGGCCGACTCTGTGATGTATAAGTCGATACCGTTCAGAGAGGACCAAGCTT
 CAAGAGAACTCAATGTGATATACAGACTGACACAGATATGGTGGATCTGATTCGATTCGAGAGATGGCCACTACGA
 TTAATGTTTTCTTGGACAGACATTTGGAAGTCTCCTCAAACTTCTCAGCATTTCAAGGAAAGTGGAATTTGGA
 AGAGGTAGTGTGGAGGAGTTGCAGATATTAAGCACTCATCAATCATCTTGAACATGGAATTTGTCTGAAGCA
 GCAACAATGTACATTTGGTTCCGAGATGAGATTAGTTGAGCTCTCTTGCACAGATGGCAGCATTTAGGGCAAGC
 TTGCGCAGACTTTGTCTTCCGACAGACCCCTACTGTGCTGGGATGGAATGCATGCTCTCGATATGCTCTCAGT
 CTTTAAAGGAGAGCTGACGCGCAGAGTGAATAATATGGCGACCAATCACCAGGTGCTGGGACATCAAGACAG
 CATTAATCATGAACCTGATGTGAAAAAGTGTATTTTGGCATTTAACTCAACCTTTCTGGAATGTATACC
 TAAATCCCAACAGCAACTATTAATGGTATATCCAGAGGTGAGGATGAGCATCGAGAGGAGTTGAAGCCCGA
 TGAAGAAATCATCAAAACGGAATATGGCTACTTGATTGGAAGTTTGCAGAGAAGGATTTGGGATGTATTACTG
 CAAAGCCAGGAGCACACTTTTCATCCACCATAGTGAAGCTGACTTTGAATGTCAATGGAATGAACAGATTTGA
 AAATACCCAGAGGGGCAGAGCATGAGGAGGGGGCAGGTCAAGGATCTATTGGCTGAGTCAAGGTTGAGATACAAAGA
 CTACATCCAAATCTTTAGCAGCCAAACCTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCCAGGAGAGAGCG
 GAGACAGAGAAACAGAGGGGGGCCAAAGTGAAGCACATGACGAGAAATGAAGAGAAACGAAATCGAAGACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTAATTTCTACTTAATTTAAAGAAAGAAATTCCTTACC
 TATAAAAACATTTGCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCATGAGTTTTTGCATAAG
 CACAAGACAAATAATCTGAATAGACAATATGTGATGAATATAAGAAAGGGGCAAAAATTTCAATTTGAACCAAGTTTT
 CCAAGAACAAATCTTGCACAAGCAAGTATAAGAAATTTATCTCAAAAATAGGGGGTTACAGTTGTAATGTTTTTA
 TGTTTTGAGTTTTGGAATTTATTTGTCATGTAAATAGTTGAGCTAAGCAAGCGCCGAATTTGATAGTGTATAAGGT
 GCTTATTTCCCTCGAATGTCATTAAGCATGGAATTTACCATGCAGTTTGCTCATGTCTTCTATGAACAGATATAT
 CATTTCTTATGAGAACAGCTACCTTGTGGTAGGGAATAAGAGGTGACACAAATTAAGCAACTCCCATATATC
 AACAGGAACTTTCTCAGTGAAGCATTTCACTCTGGAGAAATGGTATAGAGAGGTGCAATATTTCTTTCTT
 TGCCCATCGGGGTAAATTTAGTGTACTACAACATTTGATTTACTGAAGGGCAGCTAATGTTTTCCCCAGGATTTCT
 ATTCAGTGTGAGAGTAAACAGTTTACAGAGAGAAGTTGGTGTAGTTATGTTTTTTAGAGTATATCTAA
 GCTCTACAGGAGACAGATTTCTTAATAAATACTTTAATAAGATATGGGAAATTTTAAATAAACAAGAGAAACA
 TATGATGTATAATGCATCTGATGGGAAGGCATGCAGATGGGATTTGTAGAGAGAGAGAGACAGGCAT
 AAATTTCTGCTTTGGGGAAGCACTCATATCCCATGAAAGGAAGAACATACAAATAAAGTGAGAGTAAATGTAA
 TGGAGCTCTTTTCACTAGGAGTAAAGTAGCTGCCAATTTGTAATCTACTGTAAAAAAAATCTAGATTTATACA
 AACTGCTAGCAAAATCTGAGGAAGAACATAAATTTCTTCTGAAGAATCATAGGAGAGATGACATTTTATTTATAAC
 ATGATATTTTCAGTATATATTTCTCTCTTTAAAAAATATTTATCATCTCTGATATATTTCTTTTACTGC
 CTTTATCTCTCTGTATATTTGATTTGTGATATATTTTGAAGTAAAGAGAAACAAATATAACACAGA
 GTATTAAGAAATGACATTTCTGGGAGTGGGATATATATTTGTGTAATCAAGACAGGATGTAAATTTTAAAC
 AACGGAAAGGCTTAAATTAACCTTTGACATCTTCACTCAACCTTTTCTCATTTGCTGAGTTAATCTGTTGTAAT
 GTAGTATTTGTTTTGTAATTTAACAATAAATAAGCCTGCTACATGT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
GSSEGLDFQTLTLLDEERGRLLLGAKDHI FLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRCLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSGLPETHHYYIRTDISEHYWLNKAKFIGTTF
IPDTYNPDDDKIYFFFFRESSQEGSTSDKTIILSRVGRVCKNDVGGQSRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVVLEE
LQIFKHSSIIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPIITQCWDIEDSISHETADEKVIIFGIEFNSTFLECI PKSQQA
TIKWYIQRSGDEHREELKPDERI IKTEYGLLIRSLQKKDSGMYCYCAQEHTFIHTIVKLTNL
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQLSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRNRHRDLDELPRAVAT
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGACAGGTCATCTGGAGCATGCCACCAGCGGGGAGACGA
 CAACTCCCGAGTGAAGCTGGGAGCAAGACTGTAAGCTGTTCTTCAGGAGCCTGGTGATATTTCCCCACCCTCC
 CTACAGCAGTTTCAGGACAGCAGGAGCTGATCAGGTGTGTGCTCGAGTGGGAGCAGAAAGGCTGCTGGCAAGA
 GTGGCTGGAGAAAGAGGTTACGGCTTGACAGCAGCGAGCTGCCGTGACTACAAGATCCGAAGCAATGGGCATC
 GGTGAGTGGGGGGGCGGACAGCTGTATGTGCACCTCTTGTCTCAGAGAAAGAGCTGAGAGAGGGGATCTTGG
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGGAGGGAAGGATTTTAAAGTTAAAGCTGTGGCCAAATAGTTAA
 GACCAAGTTTTTGGAGCTAGACCGACATAGTTTCAAATTCCTCTCTGTTCCTTGTCTGTAGCCCCAGGT
 AAGGAGTGACTTAACCTCTCTGGACTTCAATTCCTCATCACTAAAGTAGGGCCAAATATAGCAACCCACTCAT
 AGGGAAGATTAAATGACATAATGTATGTATGATGCACTAGCAAAAGTACAGTCCCATAGTAAGTCTATGCCCAAG
 TATTTCCACCCACCCCTGTTCTCTGCCCTCCCAACAGGTAAGTCAACAGCTGGAGCAGAGGGCGGACGAGGCTT
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGTTACAGGAAGTGCAGAGAGCATCCGCCGGGACAGGTGAGCC
 AGGTGAAGGGGGCTGCCCGCTGCCCTGCTCGAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGCCAGGATGAGTGGAGCAGGAGCGCGGCTCAGTGAGGCTCGGCTCTCCAGAGGCACTCTCTC
 CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGAGCGGAGAGCTCTTTGAGGAGCTGCC
 CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTTCGTATCAGGACAGGGCTGAGGATG
 AGCTGACAAATCACGGAGGTTGAGTGGCTGGAGGTCATAGAGGAGGAGATGCTGACGAATGGGTCAAGGCTCGGA
 ACCAGCACGGCAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCAGAGAGCAGCC
 AAGACAGTGACAACTCCCTCGGGGGCAGGCCACAGCATCTCTGGCAACGGCCCTAGACGTACACCCAGGACAGA
 GTGCAGAGGCTGAGCTTGTGCGGGGCACTCATCGTCTGCTGCCCGGCCAAGATGGAGTAGATGAGC
 GCTTCTGGAGAGGGGAATTTGGGGGGCGTGTGGGGTCTTCCCTCCCTGCTGCTGGGAAGAGCTCTTGGCCCC
 CAGGGCAGGCTCAACTCTCTGACCTGAACAGATGCTGGCTCCCTCTCTCCAGGCTCTCCCACTCTGGCCTGCAC
 CTACCTCTGCTGTGGATGGGCCCTCTCACCTGTCTGCTGGGACAAAGCCCTGGACTTCCCTGGGTCTCTGG
 ACATGATGGCAGCTGACCTCAGGCGGATGCTGCACACACTCCCGCGGCTTAAAGCCCGGACTCTGGCCACC
 CAGATCCCTCACCCTGAGGCGCAGGGAAGCTTGACCCCCAGTGTATGCTGCTCCCTATCTTCAAGCTGTACAG
 CCACACCATCAATGATCCAGAGCAACACAGCCAAAGCTGGAATCGCCCTTATTTCCACCGCTCACTCTCAAGGT
 GGAACCTTGGCCCTTCCACTTTCTAGAGCTGGAACCCACTCCTTTTTCCTATTTCTCTATCTCTAGGAC
 GGAACCTACTACCTTCTCTCTGTATGACCTATCTAGGGTGGTGAATGCTGGAATCTCTGGGCTGGAAACC
 ATCCATCAAGTCTCTAGTAGTCTGGGCCACCTCTTCCCAACCTGGCTCCATGACCCACCCACTCTGGATG
 CCAGGGTCACTGGGGTGGGCTGGGAGAGGAACAGGCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
 CTGTAATGGTCTGAGCGGATTTATGACAAATGAATAAAGGGCAAGAGGCCAGGCCAGGGCTGGGCTCTTGTG
 CTAAGAGGGCAGGGGGCTACGGTGTATTGCTTTAGGGGGCCACACAGGGCAGGGGCTGCTCCAGCTGCCAC
 GCTCTATCATATGAGCAGGTGTTGGGGAAGCGGGGAGGCAAGCTGTTGAGGACAGGGGAAGGAGAAGAC
 TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGTGTCCTC
 AGCTGGGGGGCAGTGCTGCTCAGTGGAGGGGAGGGCTTTCACGCCACCCACCCCTGGCCCTGCCAGCTGGTAG
 TCCATCAGCAAAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTGCTTCTGTTCAAGCTGTGTCCAGC
 TTTTCCCTCGGGCTCAGGAGACTCCTCAGCTACACTCTCCCTGCTGCTGTTAGAGACACTGAGAGAAAGGGGAGGG
 TCAACAATGAGAGACAGGAGTAGGTCTATCAGTGCCCGCCAGAGTAGAGAGCAATAGAGGCCAGGCCAGTGC
 AGTCCCGGCTGTGTTTTCCTACCTGGTATCAGAAGTGTGTGTTTCTGGCTGCCATTGGCTCTTGAAGTGG
 CAGGCCCTGGGCTTGGGCCCTCCCTCGGCCCTCAGTGTGTGCTCTGCAGAGCTTGGGGTTCCTCTCAAGT
 GCAGGGGTAGGCTGCTGCTCCTGAGTCTCTCATTTCTGATGGGGGCTGGCTAGGAGCTGGGGCTGTGGCC
 TCTCAGGGGGAGCCTCTCCATGGCAGGCATCCCTGCCCTTGGGCTGCCCTCCCGAGCCCTGACCCACCCCTG
 GTGCTGTCCCGCCACAGAGCCAGCTCCTGTCTGTGGGGAGCCATCAGGCTGTTCTGCGAGTCCATAGCGCT
 TCTCAATGTGTGTCACCCGAACTCTGGAGGGGAGGGAACACTGGGGTTAGGACCAAACTCAGAGGCTGCTGT
 GCCCTCCCTCTGACCAAGGACATCTGAGTTTGGTGGCTACTTCTGCTTGAAGTGGAGCTGAGGAGGAGGCTCTC
 AGATTGTGGGGGCAATGTGTAGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGCCAGGCCCACT
 TTTGGGATCAGGCTGATCACTGGGCCCTTACCTCAGCCCTCTTCCCTAGGACCTGAGGACCTGCCCACTGCCA
 CAGAGAACAGCTGGCTCCCTCTCGGGGGGGGCTTTTCTCTCTTGGAGCTGCCCTGACGGCAAGTGGAG
 CCGTCTTCTGCTGGCTGCAATGGATGCAAGGGGCTCAGAGCCACAGTGCATGTGTGATGATGGAGGGGGCT
 CACTCTGAGGCTGGAGGTGGCATCCACTGCAGCAGGAGGAGGGGACTGAGGTTAACTTTCCATTTCCCT
 TCTGTTTTTTTCTTACCTTCTTACGATGCTCTTAAACCCCGAAGCCCCAATTTCCCAAGCCCCATTT
 TTTCTTGTCTTATCTAATAAACTCAATATTAAAG

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFYRYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPESQSDSNPCGAEPFAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPDGKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA
 GAAGGCAGAGACAGGCGAGGCACGAAGACGGGCCACAGACAGATTCCTACAGAGGGAGAGGCCAGAGAAAGCTGCAGA
 AGACACAGGCGAGGAGAGACAAAGATCCAGGAAAGAGGGCTCAGGAGGAGAGTTTGAGAGAGCCAGACCCCTGG
 GCACCTCTCCCAAGCCCAAGGACTAAGTTTCTCCATTTCCTTAAAGCGTCTCAGCCCTCTCGAAACTTTGGC
 TCTGCACCTTTGGCAGGAGTCAAAGGCCCCAGGCTACAGAGAGGAGCTTTCAAAGCTAGGGTGTGGAGACTTGGT
 GCCTTAGACGGCCTCAGTCCCTCCAGCTGCAGTACCAGTGCCTAGTCCAGACAGGCTCGCATCCCGGGAGGAGAT
 CTGGCAGGCGCTGGCTGGGGAGGCCAACCTGCTGCTCCTGCTCCCATTTGTCCGCTCTCTGGCTGGTGTG
 CTGTCTTCTGTACTGCTGGCTCTCTCTGCTGCTCAGGCCGGCTGGCAGGCCCTCCCCGGGAGGAGGAGAT
 CGTGTTCAGAGAGACTCAACGGCAGCGCTCTGCTGGCTGGAGCGCTTCCAGGCTGTTGTGGCTTGTGA
 GGCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAAGTTCAGGGGCTGACAGTGCAGTA
 CCTGGGCCAGGCGCTGAGCTGCTGGTGGAGCAGAGCCTGGCACTACCTGACTGGCACCATTCAATGGAGATCC
 GGAGTCGTGGCATTCTGCACTGGGATGGGGAGGCCCTGTTAGGCGTGTACAATATCGGGGGGCTGAATCCA
 CCTCCAGCCCCCTGGAGGGAGGCCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCCTACGCCGGAAGAGTCC
 TGGCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCCTTTGGAAGCCCCAGCCCCAGACCCCGAAGAGCCAA
 GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAAGATGGCCGATTCCACGGTGC
 GGGCTTAAAGCGCTACCTGCTAAAGTGATGGCAGCAGCAGCCAGGCCCTTCAAGCACCCAGCATCCGCAATCC
 TGTACGCTTGTGGTGACTCGGCTAGTGATCTGGGGTTCAGGCGAGGAGGGGCCCAAGTGGGGCCAGTGTCTGC
 CCAGACCTTGGCAGCTTCTGTGCTGGCAGCGGGGCCCTCAACACCCCTGAGGACTCGGGCCCTGACCATTTGA
 CAGACCATTTCTGTTTACCGTCCAGGACCTGTGTGGAGTCTCCATTCGACACGCTGGCTGGCTGATGTGGG
 CACCGCTGTGACCCGGCTCGAGCTGTGCCATTTGGGAGGATGATGGGCTCAGTTCAGGCTTCACTGTGCTCA
 TGAACCTGGGTGATGTCTTCAACATGCTCCATGACAACTCCAAGCCATGCATCAGTTTGTAGGGCTTTGAGAC
 CTCTCGCATCTGATGGCCCTGTGATGGCTCATCTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGGCCGCT
 CATCATGACTCTCTGGACAATGGCTATGGGCAGTGTCTTTAGACAAACAGAGGGCTCATTTGCATCTGCCTGT
 GACTTTCCTGGCAGGAGCATATGATGCTGACCGCAGTGGCAGCTTCTGGGCCGAGCTCAGGCCATTTGTCC
 ACAGCTGCGCGCGCCCTGTGCTGCCCTCTGGTGCTCTGGCCACTCAATGGGCACTGCATGTGCGACGACCAACA
 CTGCGCTGGCGCCGCGCCAGCACCTCTGGGGCCCGCACAGGCTCGATGGGTGGTGGCTGCTCTCCAGGACACA
 GCTCCAGGACTTCAAATTTCCACAGGCTGGTGGCTGGGGTCTTGGGAGCCATGGGGTGACTGCTCTCGGACCTG
 TGGGGTGGTGTGCTCACTTCTCTCCGAGACTGCACGAGGCTCTCCCGCGAATGGTGCAAGTACTGTGAGGG
 CCGCGTACCCGCTTCGCTCTGCAACACTGAGGACTGCCCACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
 GTGTGCTGCTACACACCCAGCAGCCGACCTCTCAAGAGCTTCCAGGGCCCATGGACTGGGTTCTCTGCTACAC
 AGGCGTGGCCCCCAGGACCCAGTGCAACTCACCTGCCAGGCCCGGGCACTGGGCTACTATGTTGCTGGAGCC
 ACGSGTGTAGATGGGACCCCTGTTCCCGGACAGCTCTCGGCTGTGTCCAGGGCCGATGCATCCATGCTGG
 CTGTGATCGCATATTTGGCTCCAAGAGAAAGTTGACAAGTGCAATGGTGTGCGGAGGGGACGGTTTCTGTTGAG
 CAAAGCTCAGGCTCCTTCAAGAAATTACGATACGGATACAAATGTGGTCACTATCCCCGGGGGCCACCCA
 CATTTCTTCTCGGCGCAGGGGAAACCTTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
 TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGTAATGCTGGGGCAGTCAGCTTGGCTGA
 CAGCGGGGCCACTCGAGCTCAGAGACACTGTGAGGCCATGGGCCACTGGCCAGGCTTGTGACACTGCAAGTCT
 AGTGGCTGGCAACGCCAGCACACGCTCCGATACAGCTTCTCTGTGCGCCGCGGACCCCTTCAACGCCACG
 CCCCATTCCCCAGGACTGGCTGCACCGAAGAGCAGATTTGGAGATCCTTCGGCGCGCCCTGGGCGGGGAG
 GAAATAACTCCTACTTCCCGGCTGCCCTTCTGGGCAACCGGGGCTCGGACTAGCTGGGAGAAAGAGAGAGCTT
 CTGTGCTGCTCATGCTCAAGACTCAGTGGGGAGGGGCTGTGGGCTGAGACTGCCCCCTCTCTCTGCCCTTAAT
 GCGCAGGCTGGCCCTGCCCTGCTTTCTGCTGGGAGCAGTATGGTGTAGTGGTATGGAAGGGGCTCAGAGAC
 AGGCTCCATTAATCACTGCCCTCTGCCCTCGGGCTCAGAGAGGAGGGGGAAGGCAAGGAGGGGCTGGGCC
 CAGCTTATTTATTTAGTATTTATTTCACTTTATTTAGCACAGGGAAGGGGACAAGGATAGGCTGTCTGGGAA
 CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATAAGTGGT
 TGTGTATGGCTGTGTGTGTGTGTGAAATGTGTGTGTGCTTATGTATGATGACATCAACCTGTTCTGTCTTCTC
 TTCCTGAAATTTATTTTGGGAAAGAAAGTCAAGGGTAGGGTGGGCTTCAGGAGTGGAGGATATCTTTT
 TTTTTTTTCTTTCTTTCTTTCTTTTCTTTTGTGAGACAGAACTCGCTCTGCTCCGCAAGGTTTCAACATG
 CACAACTCTCGGCTCATGCATCTCGGCTCCCGGGTCAAGTGATTTGATGACATCGAGCTCTGTGAGTAGCT
 GGATTAAGGCTCTCGCCACACCGCCAGCTAATTTTGTGTTTGTGTGGAGACAGCTCGCTGATTTGTGTC
 ACCAGGCTGGAATGATTTCACTCATCTGCAACCTTCGCCACCTGGGTCCAGCAATCTCTGCTCCTCGGCTC
 CGAGTAGCTGAGATTTAGGCACTTACCACACCGCCGCTAATTTTGTATTTTGTAGTAGAGACGGGTTTCAAC
 CATGTTGGCAGGCTGGTCTCGAATCTCTGACCTTAGTGATCACTCGCTCATCTCCAAAGTCTGGGAT
 TGCCAGGCTGCTCTGGAATCTGACCTCAGGTAACTGACCTCGCTCGGCTCCCAAAGTCTGGGATTAAGG
 TGTGAGCCACACCGCGGTACATATTTTAAATGAATTTACTATTTATGTGATCTTTGGAGTCAGACG

1007407.121301

FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPRGLAGRWLWGAQPCILLPIVPLSWLVWLLLLLASLPSARLASPLPREEEIV
FPEKLNGLSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
GTYLTGTINDGPESVASLHWGEGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPNCNVKAPLGSPSPRRRAKRFAASLSRFVETLVVADDKMAAFHAGLKRYYLLTVMAA
AAKAFKHPSTRNPVSLVTVRLVILGSGEEGPQVGPSSAAQTLRSFCAWQRLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLGMADVGTVCDFPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFFPGKDYADARQCQLTFGPDSTRHCPQLPPCAALWC SGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFENIPQAGGWGPWGPWGDCSRTCGGGVQFSSRDCTRPVPRNGGKY
CEGRTRFRSCNTEDCPTGSALTFFREEQCAAYNHRTDLKFSFPGPMDWVPRYTGVAPODQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGGNPGHRSIYLAKLPDGSYALNGEYTL
MPSPTDVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTQDWLHRRQAILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CASCAGTGGTCTCTCAGTCCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTTAAATCC
AAGAAAAATATGTAATCACTTAAAGATTGTGGACTGGTGTGGTATCCTGGCCCTAACTCT
AATTGTCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGAC
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAATTGATCCTGTG
ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACT
TAAAAACGGATACACTGGCATTCTACTCGTGGGTCTTCAAAATGTTTTATCAAACTCAGA
TTAAAGTGATTTCTGAATTTTCTGAACCAAGAGGAAATAGATGGAATGAAGAATTAACC
ACAACCTTTCTTGAACAGTCACTGATTTTGGGTCCAGCAGAAAGCCTATTGTAAACCGAGA
TTTTCTTAAAAAATCCAAAATTTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAAGT
AGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAATGACTATACTG
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
CGAGGCAACCGCTATTGCCGCCCGCTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAACCTGGTGGGTGGCCC
GCATGCTGGGGAGGGGTCT**TA**ATAGGAGGTTTGAGCTCAATGCTTAACTGCTGGCAACATAT
ATAAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCGTGAGCCAGCT
CTCCAGAAATTACTGTAGTAATTCTCTCTTCAATGTTCTAATAAACTTCTACATTATCACC
AAAAAATAAAAAAAAAA

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTTLIVLFWGSKHFWPEVPPKAY
DMEHTFFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKT
QIKVIEPEFSEPEEEIDENEEITTTFFEQSVIWWVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLDERGYCCIIYCRGNRYCRRVCEPLLGYYYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAAGTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGACCAATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCTCTGGGCATGGTGGGCACGTTGATCACCAACATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
 GCGCCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
 ACCTTTGGCATCCTCGGCGGCACCTCTTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCTGCTTTGCCTGTCTGCCAGGACGAGGCACCTACAGGCCCTACCAGGCCCGGCC
 CAGGGCCACCACGACCACTGCAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
 TGAATCCCCACAGCCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGACTGTC
 AATGGAGGCAGGGGTTCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAÀAATCCTGTCTGTTTTTGTATTATTATATATAT
 TTATGTGGGTGATTGATAACAAGTTTAAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
 TGTTTGTGATCCAGGAATAAACCTTGC GGATGTGGCTGTTTATGAAAAAAAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSPGMKFEIGQALYLGFISSSLSLIGGTLCLSCQ
DEAPYRPFYQAPPRAATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:**Signal peptide:**

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

GAGTCTCCCTCAGGAGCGGTAGCTTACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCC
CAGGCGGCAGGCGGGCGGCCAGGATC**ATGT**CCACCACCACATGCCAAGTGGTGGCGTTCCT
CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGCCACCGGGATGGACATGTGGAGACCC
AGGACCTGTACGACAACCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
GTGAGGCAGAGTTTCAGGCTTACCAGATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC
CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCCTCC
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGC
AACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
GTCTGTGTTTGCCAAACATGCTGGTGACTAACTTCTGGATGCCAGCATTAACATGTACCCG
GCATGGTGGGATGGTGCAGCTGTTACAGCAGGTACACATTGGTGCGCGCTCTGTTCTGCTG
GGCTGGGTGCTGGAGGCTCACAATAA**TT**GGGGGTGTGATGATGTGCATCGCCTGCCGGGG
CCTGGCACCAAGAAGAAACCAACTACAAGCGTTTCTTATCATGCGCTCAGGCCACAGTGTG
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG
ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCAGGACTA
TGTG**TA**ATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCGGAGAGCTCACCACAAA
AACAAGGAGATCCCATCTAGATTCTTCTTGCTTTTGACTCAGAGCTGGAAGTTAGAAAAGC
CTCGATTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCCTCAGTCTCTGTCTCTAAATATCC
ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
TCTTTTTTTTAAATATAA**CT**TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCAC
ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCTTAGTCAATAAACCCATTGATGATCA
TTTCCAGCTTATCCCAAGAAAACTTTTGAAAGGAAGAGTAGACCCAAGATGTTATTTT
CTGCTGTTTGAATTGTTGCTCTCCCAACCCCAACTTGGCTAGTAGATAA**CA**CTTACTAGGAA
GAGCAATAAGGAAAGGATATTTGTAATCTCTCAGCCCATGATCTCGGTTTTCTTACACTG
TGATCTTAAAGTTACCAAAACCAAGTCATTTTCAGTTTGAGGCAACCAAA**CC**TTTCTACTG
CTGTTGACATCTTCTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
TCCTCTTTCTGTGCGGGGTGAGAAATGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAT
TTAAGTCTTAAATATAGTTAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAAT**T**GCTTTGACATTGTCT
ATATGGTACTTTGTAAAGTCATGCTTAAAGTACAATTCATGAAAAGCTCACACCTGTAATC
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG
GGCAACATGGAGAAGCCCTGTCTCTACAAAAATACAGAGAGAAAAATCAGCCAGTCATGGTG
GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCAGGG
AGGTTGGGGCTGAGCTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCAGAA
TCTGTCTTAAAAAATAAAAAATAAATAGGAACACAGCAAGTCTTAGGAAGTAGGTTAA
CTAATCTTTAA

FIGURE 186

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVQRSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAAACCTGCTTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAAACATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTATCGCTCAGTGG
 AGAGTGTGCGGCTTCATTGAAAAACAACATCGTGGTTTTTGAAAACTTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTGCTGG
 CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCTTTC
 TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGACAAATGAGAA
 GGTGAAGGCTCACATTCTGTGTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTGGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT
 GATTGTTGGAGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACCTTCCCATCGCACACCCAAAAAGTTATCACACGGAAAGAAGTCAACCG
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTAACTTTACTATAAAGC
 CATGCAAAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAGAACTTTGATTTA
 CTGTTCTTAAGTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA
 GCTATTTTCAGCAGAATGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTTCTAAGTGGTTCAAGCATCTACTCTTTTTATCATTTACTTCAAATGACATTGCT
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATGTTTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGA
 AGATTAAATGAAGGCTTTAATCAGCATGTAAAGGAAATGAATGGCTTTCTGATATGCTG
 TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCTCTTCTCCAGAGGCTTTTTTT
 TTCTTGTGTATTAATAATTAACATTTTTTAAACGCAGATATTTGTCAAGGGGCTTTGCATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAAATATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATATTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTGTGCTTACCAAAAAACAACA
 ACAAAAAAAGTTGTCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATG
 TCATTTTTGTTCTGTGAAAAATAAATTTTCCTTCTGTACCATTCTGTTTAGTTTTACTAA
 ATCTGTAATACTGTATTTTTCTGTTTATCCAAATTTGATGAAACTGACAATCCAATTTGA
 AAGTTTGTGTCGAGCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA
 TTAATAAATTTGACATTTTTCTAATT

FIGURE 188

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPIVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCC**AT**GGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
 CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTGCGTGGTGCAGAGCACCGGCC
 AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
 GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTGCGCTTGTGGTGTACCTTGTGGGGC
 CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCTGGTGTCTACCTCTGGGA
 TTGTCTTTGTATCTCAGGGGTCTGACGCTAATCCCCGTGTGTGGACGGCGCATGCCATC
 ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCTCCCT
 CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGTGGGTGGGGGGTGTGTGTGTGCACTT
 GCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCT
 GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCT**TG**ACGTGGAGGGGAATG
 GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGTT
 CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTCTTTTACTGAGGATATTTAAAATTCAATTT
 GAAAACTGAGCCAAGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCCTGG
 ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCATCTTAGAAGC
 CAGTCAAGCTATGAACTAATGCGGAGGCTGCTTGTGTGTGCTGGCTTTGCAACAAGACAGAC
 TGTCCCCAAGAGTTCTGTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
 CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAATCATCTG
 TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCTCCGCTCTGATAAGACG
 TCCACCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
 CTTCTGCCCTGCCCCCTCGTCTCACCCCTTTACACTCACATTTTATCAATAAAGCATG
 TTTTGTAGTGCA

FIGURE 190

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLVALLFGLLVLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIRDFYNPLVAEAQKRELGLASLYLGWAASGLLLGGGLLCCTCP
SGGSQGPPSHYMARYSTSAPPAISRGPPSEYPTKNYV

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
 AGCATCTTCTACCACCTCCGAATTGAACCACTCTTCAAAGTAAAGGCAATGGCATTATATCCC
 TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCCTGGCATGTTGGGGACTCTTGCCACAACCTT
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
 TGGGAAGGGCTCTGGATGAAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGTCTCTTGTGGCTCTCCCGCCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
 GGCTCTAACGAGAGGGCCAAAGCATAACCTTCTGGGAACTTCAGAGTCCCTCTTCATCCTGAC
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA
 ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCTTGGCTGGGCA
 AGCGCTGCTGTCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCACTTATGTCTAAATGCCTCCTTTTGGCTCCAAGT
 ATGGACTATGGTCAATGTTTTTATAAAGTCTGCTAGAAAAGTAAAGTATGTGAGGCAGGA
 GAACCTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAATGCATTGACTATTGTTG
 GACCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
 TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA
 GTTGAAATTGATATTCTATAACAATAAACATATACCTATTCTA

FIGURE 192

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRD FYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV

Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAACTCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
CATACCTACCAGTTTGTGGTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTTCAGTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTTCAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCCAGA

FIGURE 194

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVVYFCSSSEAAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC
```

Signal peptide:

amino acids 1-19

197/249

FIGURE 195

CCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCC**ATG**GCTGCCTCCCCGCGCGGCCTGCTGTCTTGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAGA
ATTCCCTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCTACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACT**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCT
CTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTCAGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAATAAAGCATTTTGTAAAAAGA

FIGURE 196

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLLLCWGGISGNKLLMLQKREAPVPTKTKVAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYG DY QRHYD
EDSAIGPRSPYGFRHGASVNYDDY
```

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCCGCCCGGAAGTCCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC
GGTAGCGCGGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGTGGGTGATGAGGTGAC
CGTCCTTTTCTCGGTGCTTGCTGCCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCAGCCCAGC
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCGACCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTACAGCAACACCGCCAG
CCCCGGACTCCCCGCGAGGAGCCCCCTCGTGCTACGGCTGAAATTCTCAATGATTACAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAGGACCCAGTTTCCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
CCAAATCCCCCTGCCCCGCGGGTCCGAGCCCGGCCCTCCGGGCTGGAATCGGCAGCCT
GCTGCTGCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTTCCCTGACCGCCACTCTGGGCTGGCCGGCTTACCCCTGCTCCTCAGTCTCCTG
GCCTTTGCCATGTACCGCCCG**TAGT**GCCTCCGCGGGCGCTTGGCAGCGTCGCCGGGCCCTCC
GGACCTTGCTCCCCGCGCGCGGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG
CCTCTTCCGCTGCCCTGGAGCCAGCCCTGCGCGCAGAGGACTCCCGGGACTGCGCGGAGG
CCCCGCCCTGCGACCGCGCGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
CTGGGAGTGGGCTCCTCGGGGTCGGGCATCTGCTGTCGCTGCCTCGGCCCCGGGCAGAGCCG
GGCCGCCCGGGGGCCCTTAGTGTTCTGCCGAGGACCCAGCCGCCCTCCAATCCCTGAC
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTGCGTGGGAGGCTGGTGAAGGGGAGCGGGGAG
GGGCAGAGGAGTTCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAA
AAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCV LHCHVSTRVGPFPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCCTCCCTCCAAGGATGACAAAGCGCTACTCATCTATTTGGTCAGCAGC
TTTCTTGGCCATAATCAGGCCAGCCTCATCAGTCGCTGTGACTTTGGCCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTTGAGGGTTACTCCTGAGTGACTGCGTGTGCCTGGCTTTTGTGG
AAAGCAAGTTCACATATCAAAAGATAAAATGAAATGCGGATGGAAGCTTTGACTATGGCCCTC
TTCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGGCATCCACTGCGCAAAAAGGA
TTGTGTCCGGAGCACGGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTCAAGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATGGAACAGGGTGCGGGTGACCCGTGG
AGTCATTCCAAGACTCCTGTCTCTACTCAGGGATTCTTCATTCTTCTTCTCTACTGCCTCCA
CTTCATTGTATTTCTTCCCTTCCCAATTACAACATAAACTGACCAAGAGCCCCAGGAATAAA
TGGTTTCTTGAGGTTCTCCTCTTCACTCCCATCTGGACCCAGTCCCGTGTTCTGTCTGTTAT
TTGTAACCTGGAGACCACAATAAGAAATCTTTATATTTATCG

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSLENLCHVDCQDLLNPNLLAGIHC AKRIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

CTTGACCTGACTGGAGCGCTCAAAGAGGGACGGCTGTCAAGCCCTGCTTGACTGAGAACCACA
CCAGCTCATCCCCAGATCTTCATGCAACCTATTATACAAAGGGGGAGGAACCACTGAG
CAGAAATGGAATCATATTATTTTCCCAAGGATGAACACCGGGGTAAAGGAGGGAACCAATT
AATTTGAAGTCCCTGTGAATGGGCTTTCAAGAACCAATTAAAGAAATCCCATCAGAGAGAC
TTGGGTTGAAACTTGGGCTCTGTGTTTTCTGATTGTAAAGTGAAGCAGGTTCTGCACAGCG
TGTGTCGAATGTCAGGACCAAGGTTAAGTGAATGGCAGAAAACTTCCAGGTGGAACAAGCA
ACCATGTTCTGTCTGCAAGCTGTGAAGGAGCTGGAGCGGGAGGAAGCTAATCTGAACATGAC
CTGTGTCAATTTGGCAAGTTCTAGCAACA**TGCT**CTCAAGGAAGCATCAGGCCACAGCAAT
CAGACTCCAGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCTGATGATGGTGGCAGTGT
TGACCCCTCCCCACACCACTGCACAGCACTGTCAACAGCCCAAGCCAGGACAGCAGCTGT
GAAGCCAGATACCGCTGGACTTTGGGGAATCCCAAGGATTTGGTGAAGTGAAGCTGAGGATGA
GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCTTTATCTCTACTGCGGGAGGATCAGC
TGTGGTGGCCCTGAGGCTTACCCCAGGCGAGAAGGAACCAAGCCAGGCGAGGAGAGGTTGG
AGCTACCGCCTCATCAAGCAGCCAAGGAGGAGGAGTAAGGAAGCCCAAGAGGGAGCTGGG
GGGTGATAGGAGCGGGGAGGTTCTCTGAAGAGAGGAGGTTGACCCGTTTCAGCTGCGAGCCAC
GTGGCTCTCAGGAGGACCTAGTGGCCGATCCCCCTCAGGAGGGCTCTGCCCGAGTGGCG
CACCACATGTGTCTGCAGCAGCAACCTCAGGACAGCTGCCACAGCCAGCGCTCATCTGT
TTTCCATGATGAGGCTGGGTCACCTCTCTCGGAGCTGTACACAGCATCTCGACACTGTG
CCAGGGCTTCTCTGAAGAGATCATCTCTGTGCAGCACTCAGCCAGCAAGGACCACTCAAG
TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGTTGAAGTTACTCAGGACAACAAGAG
GCTGGTGCCTCAGGGCCCGGATGTGGGGGCCACCAAGCAGCCAGGGGATGTGCTGCTCT
FCATGGATGCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCTCAGCAGAATAGCT
GGTGACAGGAGCCGAGTGGTATCTCCGGTGTAGATGTGATTGACTGGAAGACTTTCGGAAT
TTACCCCTCAAAGGAGCTCAGCGTGGGGTGTGTGAGCTGGAAGCTGATTTCCACTGGGAAC
CTTTGCGAGGACATGTAGGAAGGCCCTCAGTCCCCATAAGCCCATCAGGAGCGCTGTG
GTGCCGGAGAGGTTGGTGGCCATGGACAGCACTTATCCAAACACTGGAGCGTATGACTC
TCTTATGTGCTGCGAGGTGGTGAACCCCTCGAATCTGCTTTCAAGGCCCTGGCTCTGTGGTG
GCTCTGTGGAATCTCTTCCCTGCTCTCGGTTAGGACACATCTACAAATCAGGATTTCCAT
TCCCCCTGCACAGGAGGCCACCTTGAGGAACAGGGTTGCAATGTGCTGAGACTGGCTGGG
GTCAATTCAAAGAACCTTCTACAAGCATAGCCAGAGGCTTCTCCTTGAGCAAGGCTGAGA
AGCCAGAGCTGCATGGAACGCTTGACGCTGCAAAAGGAGCTGGGTTGTCGGACATCCCACTGG
TTTCTGGCTAATGTCTACCTTGAGCTGATACCCATCTGAACCCAGGCCCGATTTCTCTGAAA
GCTCCACAACGATGGACTTGGGCTCTGTGAGCATGCGCAGGACAGGAGGGAACATCTGGCT
GTCCATGTGTTGGTCTCTTGCAGTGAAGCCGCGACCAAGTCACTGCAGCACAACGAG
AGGAAGGAGATTCACTTTGGCAGCCACAGCACCTGTGCTTTGCTGTCAAGCAGGAGCAGGT
GATTTCTCAGAATCTGCACGGAGGAAGGCCCTGGCCATCCACGAGCAGCATGGGACTCTCAGG
AGAAATGGGATGATTGTCCACATTTCTTTGGAAATGCAATGGAAGCTGTGGTGCAGAAACAA
AATAAAGATTGTGATCTGCGTCCGTGTGATGAAAAAGCCCGCAGCATGGCGATTGTGACCA
GATAAATGCTGTGAGTGAACGAT**GAA**TGCAATGTGCAAGGAAAGAAAGAAATTTGGCCATC
AAAAATCCAGCTCCAAGTGAAGCTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTGTGT
GTGCTCTCTTTGTGGTAGGAGGAAAAAAGCTCATGAAGAGATATAGGAAGTTTCTCCTTT
TGACACCTATTGTTCAATGACGTCTGGCTCTTA

FIGURE 202

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRWDGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRGLAIRARMLGATRATGDVLFVMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFOYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSEILPCSRVGHYQNDSSHSPLDQEATL
RNRVRIAETWLGSEFKETFYKHSPEAFSLSKAEKPDCEMERLQLQRRLCRTFWHFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCAEGDILGCPMVLAPCSDSRQQQYLYQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQHWDQENGMIHVILSGKCMEEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER
```

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTCACAGCTGAGGAAGACCTCAGAC**ATGGA**
 GTCCAGGATGTGGCCTGCGGTGCTGCTGTCCACCTCCTCCCTCTCTGGCCACTGCTGTTGCG
 TGCCCTCCACCACCGCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACCAGCCCCAGCCG
 CGCCCCCGGTGTGCCAGGGGAGGCCCTCGGCCACGTCATGTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGCGCAAGTCTGCCTGGCACTG
 CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT
 ATCTGTGGGGTCCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCACTCTGCCAATCCCGG
 ATTTCTGGACTATGGTTTTCTGAGCCCTCATGGGCTCGCAACCCACACCTCCCACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCTGCGGCCATT
 CTGTTGCGGGGCGGTGGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCCGAGCCAGAAGC
 GACGCAGACCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCTTCGGGGACTCACCTACCCCCACCCC
 TGACCATGAGGAGCCCCGAGGGGACCCCGGCTGGGATGCCCCACCCCAAGGGGGCTCCAG
 CCTTCCAGTTGAACCGG**TGA**GGGCAGGGGCAATGGGATGGGAGGAGGAAGAGGGGAAGGCAC
 TTAGGCTTTCAGAGCTGGGGTGGGGTGCCCTCTGGATGGGTAGTGAGGAGCGAGCGCTGGC
 CTCACACGCCCTTGCCCTTCCCAAGGGGGCTGGACCACTCTCTCTGGGAGGCACCCCTTC
 CTTCTCCAGTCTCTCAGGATCTGTGTCTATTCTCTGCTGCCATAACTCCAACCTCTGCC
 TCTTTGGTTTTTTCTCATGCCACCTTGCTAAGACAACCTGCGCTCTTAACCTTGATTCCC
 CCTCTTTGCTTGAACCTTCCCTTCTATTCTGGCTTACCCTTGGTTCTGACTGTGCCCTT
 TCCCTCTTCTCTCAGGATTTCCCTGGTGAATCTGTGATGCCCAATGTTGGGGTGCAGCC
 AAGCAGGAGGCCAAGGGGCGGCACAGCCCCATCCCATGAGGGTGGGGCAGCTGTGGGA
 GCTGGGGCCACAGGGGCTCTGGCTCCTGCCCTTGACACACCACCCGAACACTCCCCAGCC
 TCACGGCAATCCTATCTGCTGCCCTCTGCAAGTGGGGGCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCTTGTGCACTCACATGAAGCCTTGCACTACCTCCACCTTCAC
 AGGCCATTTCGACACGCTCTGCAACCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCTCGTCTACATTGCACTCTCTCTTCCACATTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTCTGCACTTTACCTCTCATGTGCGTTTCCCGGCTGATGTTGTGGTGG
 TGTGCGCGGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGAGCCCCG
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTATGG
 TCTCGTCCCATTCACACCAATTTGTTTCTCTGCTCTCCCATCTACTCCAAGGATGCCGGCA
 TCACCTGAGGGCTCCCCCTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCAGCCCA
 CTGCTAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCTGCTGCACTACATGAGAA
 AGGGACTCCCATTTGCCCTTCCCTTCTCTACAGTCCCTTTTGTCTGTCTGTCTCGGCTG
 TCTGTGTGTGGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCTCCTTCCCAGCT
 CCCTTTGGGCTCCCTAACTCCACCTAGGCTGCCAGGACCGGAGTCACTGGTTTCAAGGCC
 ATCGGGAGCTCTGCCCTCAAGTCTACCTTCCCTTCCCGACTCCCTCTGTTCCCTTCTTT
 CCTCCCTCCTTCCCTTCCACTCTCTTCTCTTTTGTCTTCCCTGCGCTTTCCTCCCTCCTCAGGTT
 CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCTCTCTTCCCTTCTCCCTGGCTCCTAGGCT
 GTGATATATATTTTTGTATTATCTCTTTCTCTTCTTGTGGTGATCTTGAATTACTGTG
 GGATGTAAGTTTCAAATTTTCAAATAAGCCTTTGCAAGATAA

FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGFAASFPQRLRGLLLLLLLQLPAPSSASEIPKGKQKQLRQREVVDLYNGMCLQGPA
PGRDGSPGANVIPGTPGIPGRDGFKEGEGCLRESFEESWTFPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGG**ATGG**
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
CAGCCCCACCGTCGCGCCAGGACCCGAGGACAGCACCAGCGCAGGAGCGGCTGGACACGGGC
GGCGGGTCGCTGGGGCCCGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCGTGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA
GGGGCCGCGCCCGCCGCGCGCGACTCGGCAAAAAAAAAAAAAA

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FIGURE 206

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
>subunit 1 of 1, 121 aa, 1 stop
>MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

GCGCGTTGGTTGGTGC GCGGCTGAAGGTTGTGGCGAGCAGCGTCTGTTGGTTGCCCGCGC
 CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCTTGGTGTGCTTACGGCGCGCTGGCCCA
 CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACGGCCACCATTGTA
 ACTTCAAGTCTCTGGTGGGTGGGCACATCCCCGTGTACAGGGCGCTGCTACCCGACTGGAG
 GACGACACGATGAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
 CCGGGTATTTCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAA
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCCTAAGTAGCC
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 CGACTGTACAGCACCGTGTGGCATCTTCCAGTAGCAGACCATCTCCTGCAACAACCTGCACAG
 ACTCGCACGTCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
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 CCTGGGACACACAGAGCCACCCCGGCTTGTGAGTGACCCAGAGAAGGGAGGCCCTCGGAGA
 AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGCCTGCACACCCTTCGACATCCACGGC
 ACGAGGGTGTCTGGATGTGGCCACACATAGGACCACACGTCACGCTGGGAGGAGAGGCCT
 GGGGCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
 CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
 TGAAGATGCTGTGAGTGTCTAAGCAGCACTGACAGCAGCTGGGCCTGCCACAGGGCAAC
 GTGGGGGCGGAGACTCAGCTGGACAGCCCCTGCTGTCACTCTGGAGCTGGGCTGCTGCTGC
 CTCAGGACCCCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGAG
 GAGGGAATGGGGTGGGCTGTCTGCGCAGCATCAGCGCCTGGCAGGTCCGACAGCTGCGGGA
 TGTGATTAAGTCCCTGATGTTTCTC

FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
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FIGURE 209

AGCAGGAGCAGGAGAGGGACA**AATG**GAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATTGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCACTACTCCA
 TAGCATGGTGCAAAAATTCACAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCCGCTGGTAGACAATGAACAACGT
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCTGTGACTGTGATTGGGTATTCAACAGCG
 TAATTCAGATTTCCTCTCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTTCTGGTGGACAG
 TGGTATGAAGAAAAATGGGAAGGTGATATCATTTTCAAACCTAAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCTTAAGTGGAATAATGTTGAAGAAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**CTGAC**TTCTCCTTGGAACCTACATATGGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACCACACACACACGACGTCACACACGACGACGCGTGCACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCCTGTCTTAAAAATCTCGTTTTCTC
 TTCTTCTCTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCAAT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTTGTCAATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTCTGCTCTTTTAAAGGTTACCTAAGGT
 TGAACTCTACCTTCTTTTCATAAGCATGTCCGTCTCTGACTCAGGATCAAAACCAAAAGG
 ATGGTTTTAAACACCTTTGTGAAATGTCTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCC
 TATGTAAATCAACAACCTGCATAATAAATAAAAGGAATCATGTTATA

FIGURE 210

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAEEVAAEEVEKSSDGFGAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRDVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLILLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDWDTLPTAEVSVVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
GACGCGGCGGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATGG**CAGCGTCCGCCGAGCCGGG
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTCTGGCGGCGGCGCTTGG
GCTCTTGACAGCTGGAGTATCAGCCTTGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAGTCTACTAGTACGACTGGCGGGTTGACC
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTC
CCAAGGGCAAGTGATCACTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
TATATCTGTGATGTCAAAAACCCCTCTGACATCGTTGTCAGCCTGGACACATTAGGCTCTA
TGTCGTAGAAAAAGAGAAATTTGCCTGTGTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
CTGTGGTCTAGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGC
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
AGGGCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC
CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGT
AGCCTTGGAGACCCAGGCAAGGACAAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
ACAAAGGATATGTATAAATATCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA
TGAAAAGATGGTATGATTCTAÇATATGTACCCATTGTCTTGCTGTTTTGTACTTTCTTTTC
AGGTCATTTACAATTGGGAGATTTCAGAAACATTCCTTTACCATCATTTAGAAATGGTTTG
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
GGCTTAAGACTGATTAGTCTTAGCATTTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAA
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG
AAATGTGTATATCAATTTCTGGATTATAATAGCAAGATTAGCAAGGATAAATGCCGAAG
GTCACTTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTT
GAGAACTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTTA

FIGURE 212

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASININ
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCGSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHSDKINKSESVVYADIRKN
```

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCC
 CCCGGGGGCTTGGCCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCGGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGCGGGGCCCTCGGGCTGGGGCTGGGGCTGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGGGCCCCGGCGCAGTCCCCCGCGCCCCGACCTTGAGGCG
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC
 GCCGCCCTGCTCCAGGTGCTTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATTGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGTCACAACAAGATTACTGATTTCCCATTTAAGTGGAAATTCG
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
 TGAAGAGAATGTTGCATTGAGCAAGAAAAAGAAGCAGAAAGTAATGAAAAGAATGATTTT
 ACTAAATTTAAAAAGAGCAGGAGGAATGAAGCCAAATGCCGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGCGAATTATATTGAGAGAAAAGTTTGAAAATTC AATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
 ACTTTTGCTATACCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA
 CTATATGCAGAAAATATTCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTTACAATAGAGCAAGGTAAATGAATACCTTCTGCTGTGCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTTAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGCTGTTTCTCATCTGTAAAGTGAAGGAAGTAAAAACA
 TGTTTATAAAGTAAAAAAA

FIGURE 214

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVCKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
 AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT
 GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTTCGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTCCGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCTCGTCTGTTCTCCTCATGATGTCAGG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTTCAGAAACCCAG
 GAATGGCTGTCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
 TAAACTGTCCCCCAGATCGACACGCAAAAAAAA

FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLMAVAAPSRRGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGLRDVAALNGLYRVRIPRRPGALDGLEA
GGYVSSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPEATAAFIERLEMEQAQKAKNPQEQKSFFAKYWYIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGGSLCCVPPSI

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

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FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGAGCCGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCGCAGACCAGGGGAGCAGGTGCTCCGGGGGCCACC
ATGCTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGCCTGCAGCAATCCCTCCTTCCCTTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTAATACTTCCTGGAAGGTCAAATTGCCATCCTCTATGCTG
 TGGCCTTGCCCTACAGTCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC
 GCAAGAATTCTTGTGCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT
 CAAGACTACTTTGTGCTGCTAGTGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC
 GGCAGCGTGCCCTTCTCAAGGACCTGTGCTGGAGGCCCTGCGCTGCCTCCTGTGCGACCGCCGC
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTCACTTTCATCTTTGTCTTCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGTGTGCTCATCGTCGTCTTCTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCCTTCATAGCCTTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
 CCTTGCTCCTCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTTACGATTTGCTCTG
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTCACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTTACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATCCAGCTATCCGGGATTGTACAGATCTCTCTGT
 GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGGTGATGGACTGGAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAA
 ATAAACACTTTTAAATGATCAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDYQVYFLALAADWLQAPY
 LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
 QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
 VAAEAVASWIGLGPVAPFVAAIPLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
 VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSFMAASLLGSSLYRIATSKRYHLQ
 PMHLLSLAVLIVVFSLSFMLTFSTSPGQESPVESFIAFLLLIELACGLYFSPMSFLRRKVI PET
 EQAGVLNWFRVPLHSLACLGLLVLHDSDRKTGTRNMFSCSAVMVMALLAVVGLFTTVVRHDA
 ELRVSPSTEOPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
 314-330, 343-359, 379-394, 410-430

GCGACGCGCGCGGGGCGGCGAGAGGAAACGCGGCGCGGGCCGGGCCCTGGAGATG
GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCCTCGCGGCCA
CGGCTTCCGTATCCATGATTATTTTGACTTTCAAGTGCTGAGTCTGGGGACATTCGATACA
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
CACCTTGTCCCCGCTGAACCTCCAGAGCGCTCGCGGGAACTCAGCAACGGTTTCTTCATCCA
GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAAGTGTGCAATGACAGCTTCTAC
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTGCTCGG
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
CCATCCCAGTCAATGTACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGGTAGAAGAGTTTGTCCACATTCACGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
AGGAATTTTGCTACTTGGAAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG
GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
GAACCCGAAAAAAAAGGAGCTGAAGCAGGTTGCCCTGAGAGGCATCTGTGACCTGTCACAT
CAGCTGGCTCAAGCCTCCCCTACCCAGGGTCTCTGCACAGTACCTTCACAGCAGTTGTGTGG
AGTGGTTTAAAGAGCTGGTGTTTGGGGACTCAATTAACCCCTACTGACTTTTATGCAATAAA
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNQFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISTPVNVTSIPTFELLQPPWTFW
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Signal peptide:

amino acids 1-20

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FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATCCATGGAACTTGCCTGCTGTGTGGGCTGGTGGTGA
 TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
 ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG
 AGGCCAACCCAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTGCTATGACCACC
 TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAGCAGCATACATTGTATGGAT
 TTATCTCAACGCTATTGTTTAATGGCTGTGTTTAAATGTGATCTATCTGGAAAATGAGGACTC
 CGAATAAAAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIFIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQCGGIYKDNNKSSIHCMDSLQRYCLMAVFNVIIYLENEDSE
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCCTTCTGGATGGGGGCCAGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTACGACCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACACCCGTGGGTCGC**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAAA

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK
LGDSWDVKLGALGGNTQEVTLQPGYITKVVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGYQLLGIKISIGFEWNYPLEEPTTEPPVNLITYSANS PVGR
```

Signal peptide:

amino acids 1-22

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAAGTGGGTGCTCATCAGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTTGCGTGGGAAGAATACATCATGTTTTTCGATAAGAAGAAATGTAGGATCCAGTT
 TTTTTTTTAAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
 TATTTGTTCTTGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCCAAGGGGTCCAATTTTCTCCCTGGGTGTGACGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGGCTGTCTGCAACTGGCCCTTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA
 CAATACAAAGGATGGGTTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGTCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT
 CAATTTAAAGGGCTCAACCAGCTCACCTGGGTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATCTCTAGTTCCAATAGAA
 TCTCCTATTTCTTAAACAATACCTTCAGACCTGTGACAAATTTACGGAACCTTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTCGGGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
 ATGATCAGACTCAAAGAACCTTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCACTGGAATAAAATCAGTGTCTATAG
 GACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTATCAGGCAATGAGATC
 GAAGCTTTTCACTGGACCCAGTGTTTTCCAGTGTGTCCGCAATCTGCAGCGCTCAACCTGGA
 TTCCAACAAGCTCACATTTATGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTGCTCCCTGTAACTGGCTG
 AAAAGTTTTAAAGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAATACAGCATCTGTGGCAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCAT
 GAGAGCAAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG
 TGCTCGTCACTCCTGTGTTTATCTACGTGTGATGGAAGCGGTACCCTGCGAGCATGAAGCAG
 CTGCGAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAT
 GACTCCCGAGCCAGGAATTTTATGTAGATTATAAACCCACCAACAGCGAGACCGAGCGAGA
 TGCTGCTGAATGGGACGGGACCTGCACCTATAACAATCGGGCTCCAGGGAGTGTGAGGTA
 TGAACCATTTGTGATAAAAGAGCTCTTAAAGCTGGGAAATAAAGTGGTGCTTTATTGAACCT
 TGGTGACTATCAAGGGAACGGGATGCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG
 CAAGATCCTTCTCTGTCCGTTTTAGTGCAATTCATAATACTGGTCAATTTTCTCTCATACATA
 ATCAACCCATTGAAATTTAAATACCAATCAATGTGAAGCTTGAACCTCCGTTTAAATATA
 TACCTATTGTATAAGACCTTTACTGATTCCATTAAAGTTCGCAATTTGTTTAAAGATAAACT
 TCTTTCATAGGTAAAAAATAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTVLTLMLSSAERGCPCGRCGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRI SYF
LNNTRFPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRITIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKEHLHLEHNQFSKLNLLALFPRLVSLQNLVYLQWNKISVIGQTM
SWTWSSLQRLDLGSGNEIEAFSGSPVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKKIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMPSTQEFYVDYKPTNTTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACCTATCCTAAGTTGACTGTCCTT
 TAAAT**ATGT**CAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
 TGTTCGCCGTATTCCAGTTGGTGTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCTCTGCCTCCAGTGTGGCTGAGGAGACCCCGA
 ATTGATTCCTCACAGGCGACCATGGCAGTTTTTGTCTGTTGGAGACTTGGACTCTATTTATGG
 GACAGAAGCAGCTGTGAGTCCAACGTGTGGAATTACCTTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
 AAAACAACCT**TGA**TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATCCA
 AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
 GTCTGAGGAAGGACAATTCGACAAAAGATGGATGTTGGAAAAAATTTTGGTCATGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
 AACCAAATTAATGCTTCTCCACTAGTATCCAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
 CTAGCATGGGGTCCATAAAAATTATTATAATTTAACATAGCCCAAGCCGAGAATCCAACAT
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
 CTTTTACAGTAATGAATGTGGCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG
 GCATTTATTGCAGCATCATGCTAAGAACCCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGACAGA
 CAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
 AAACATCAATAGATATCTAAAAA

FIGURE 228

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDMCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAAACTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCGAGCTGACGCCCGCTTATTA
 GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGACCGTGACGAGAAGCCC
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT
 CCCTCTTCAAAACTCATCTCTGGGTGACTGAGTTAATAGAGTGGATACAACTTGCTGAAG
 ATGAAGAATATACAAATATTGAGGATATTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGC
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTA
 CAATCTCAAGAAAAATATGTCCAGAAATTGAGTTTACTGTGCTTGTATTTGGACTCATTT
 TGGGATTGATGTTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAACTACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAATAAGA
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGCGAGGATATGCGGATCTGAAAAGAACAAATT
 GCTGTCCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTGTGAATGGCTCAGCAGCCAAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
 CCACAAAATAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAAACACCTTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
 AGAGCAATACCTTTACAATAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCAATGGAAC
 TCTAATTTCTGTACATAAAAAATTTTAAAGTTAATTTGTTTGCTTTTCAAGGCAAGTCTGTTCAATG
 CTGTACTATGTCCTTAAAGAGAAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATTCT
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTTGGACAAGTGAAGAAATGTTTAA
 TCATTTCTGTCATTTGTTCTCAATAGATGTAACGTGTAGACTACGGCTATTTGAAAAATGTG
 CTTATGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAAATGTATTGATTTGCACATATCCTTCAGAAATACTGA
 AGGTTAATATTGTATATTTTAAAAAATTACCTTATAAGAGTATAATCTTGAAGTGGGTAG
 CAGCCACTGTCATTAGCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAAATAGTT
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAGATATTTTATGATGAGAGTAACAATA
 AAGTATTCATGATTTTTTACATACATGAATGTTCAATTTAAAGTTAATCCTTTGAGTGCTCT
 ATGCTATCAGGAAAGCACATTATTTCATATTGGGTTAATTTTGCTTTTATTATATTGGTCT
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAA
 GGTACTTTTGTGCTGCATTAATTTGCTTGGAAAGTGTAAACATTATATTATATAAGAGTATC
 CTTTATGAAATTTTGATTTGTATAACAGATGCATTAGATATTCAATTTATATAATGGCCAC
 TTAATAATAAGAACATTTAAAAATATAAATGAACTATGAAGATTGACTATCTTTTCAGGAAAAAGCT
 GTATATAGCACAGGGAACCCCTAATCTTGGGTAATTTCTAGTATAAAACAAATTTATACTTTTAT
 TTAATTTCCCTTGTAGCAAACTCAATTGCCACATGGTGCCCTATATTTTCATAGTATTTAAT
 CTCATATGAACCTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAAATTTAGATAT
 TGTATTGTTGCTCATTATAATATGTACCACATGTAGCAATTAATACAATATTTTATTAATA
 TAAATATGTGAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTCTCTCTCTCTGTA
 CTGCTACCTTTATGGAAGAAATTAATTATATGCCATTGCCAGGT

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTNKRITNVSGSIR
```

Important features of the protein:**Signal peptide:**

amino acids 1-26

FIGURE 231

CGCGGCCGGGCCCGGGGGTGTAGCGTGCAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCGTGGCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAAACCGGCCATGCT
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG
 GTGGATTGTAGCGGCCGTGGGCCCCACATCATGCCGTGCCATCCCTCTGGACACAGCCCA
 CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTTGGCGGGGCCGGCT
 ACACGACGTGTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCTAGTGC
 TTCTCCCGCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
 AGCCGAGAGCTTCACAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG
 AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCATACAGTGGACCTCTCC
 CACAACCTCATTACCCGCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCAACAT
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC
 TGGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCAATTGGTCCGGGTGCCTTCGCGGGG
 CTGGGAGGCCTTACACACCTGTCTCTGCGCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTTCCTGAGCTACCGGGCCTGCAGGTCTCGGACCTGTCGGGCAACCCCAAGCTTAAC
 GGGCAGGAGCTGAGGTGTTTTTCAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC
 AACTTGGTGCCCTGCTGTAGGCGCTGCTCCTCCACCTCCCGGCATGCAGAGCTGCAGCTG
 GGGCCAGGATGTGCGGTGCGGGCCTGGTGGCGGAGGGCACTACCCCGGAGGCCTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC
 ATCTTGT**TGAC**AAATGGTGGGCCAGGGCCACATAACAGACTGCTGTCTGGGTGCCTCAG
 GTCCCGAGTAACCTTATGTTCAATGTGCCAACACCAAGTGGGGAGCCCGCAGGCCTATGTGGCA
 GCGTCACCAACAGGAGTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
 AAAGTCTACCCCTTTGCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA
 AACCAGACTCGGGTCCCTCTGCTTCCCTTCCCCACTTATCCCCAAGTGCCCTTCCTCAT
 GCCTGGGCGGCTGACCCGAATGGGCAGAGGGTGGGTGGGACCCCTCTGCGAGGGCAGA
 GTTCAGGTCCACTGGGCTGAGTGTCCCCCTGGGCCCCATGGCCAGTCACTCAGGGCGAGTT
 TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCGCTTCATCCTTTTCTAT
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAGAATCAAGTCCACCCTTCTCATGTGAC
 AGATGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC
 ATGACTGGAGCACAGCCTCCTGCCTCCCAGCCGGACCCCAATGCACTTTCTTGTCTCCTCTA
 ATAAGCCCCACCTCCCCGCCTGGGCTCCCTTGTGCCCTTGCTGCTGTTCCCCATTAGCACA
 GGAGTAGCAGCAGTCAAGCAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT
 GTGCGGCTAGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT
 CCAGCCTAGCCAGTTTCTCACCCCTGGGTGGGGTCCCCAGCATCCAGACTGGAAACCTACC
 CATTTTCCCTGAGCATCCTCTAGATGTGCCCAAGGAGTGTGTCAGTTCTGGAGCCCTACA
 TCTGCTGGGATCTCCAAGGGCCTTCTGGATTCACTCCCCAGTCCGCTGAGCAGGACAGC
 CCTTCTTACCCTCCAGGAATGCCGTGAAGGAGACAAAGTCTGCCCGACCATGTCTATGC
 TCTACCCCCAGGCGAGCATCTCAGCTTCGAACCCCTGGGCTGTTTCCTTAGTCTTCATTTTA
 TAAAAGTTGTGCTTTTTTAAACGGAGTGTCATTTCAACCGGCCTCCCCACCCCTGCTGGC
 CGGGGATGGAGACATGTCATTTGTAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAAAT
 ATTGTCTGGGCTGTGTTGGGGTGTGGGGAGCTGGGCATCAGTGGCCATAGGCAATC
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCCTAGC
 CCATCATCTATCTAACCGGTCTTGATTTAATAAACACTATAAAGGTTTAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1001/407-121307

FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTTTPCFPGCQCEVETFGLEFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLVLDLSGNPKLNWAGAEVFSGLSSIQELDLSGTNLVPLPEALLHLPAIQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTCGATTTCTCCCCAGTTCCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA
 AAACAAGTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCTACTGCAAGTGCTGTGT
 GTTCCAGGCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTCAC
 GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCC
 TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCCTC
 TGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCATCTCTTTACT
 GTACTAGTCTTGTGCTGGTGCAGTGATCTTATTTATGCATTACTTGCTTCCTTGCATGAT
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGATAAGATTTTGTAAATATCTT
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTCTATTTAATGTATTT
 ATTTTTTTTACTTGGACATGAAACTTTAAAAAAATTCACAGATTATTTTATAACCTGACTAG
 AGCAGGTGATGTATTTTATACAGTAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCT
 AGGGGGGTTATTCTTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
 CTTCAGCCAGGAATCTACACGGCCAGCATGTATTTCTACAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

FIGURE 234

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLWLSPDFRPKMKASSLAFSLLSAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLRLYLDRVFKNYQTP
DHYTLRKISSLANSLFTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
 CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAATGCAAGGAGAAGCAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCGCCAT
 TTACAGACACGTAGTGATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTG
 TGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACAGACCTAGTGAAGGTTTCAGATGCAAAAT
 GGAAGGAAAAAGGAACTGGAAGGAAAACCATTGCGATTTTCGTGGTGTTACATCATGCATTTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCACCTATGATACAGTGAAACACTACTTGGT
 ATTGAATACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
 TGGTAGCTTCTATCTGGGAACACCAGCCGATGTCAAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACCATCTTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTTTTAA

FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPPLDLTKTRLQMQGEAALARLGDGA
RESAPYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFVKSEDEH
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRRKLEGGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
 GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
 TTAAGAAGTAAAAATGCGCAGGCTTCTAGATAATTTTCGTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCCTT
 TCACACATGTGGTGTATTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
 TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC
 ATATGTTATCCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAAATGCACTTA
 TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC
 TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTT
 TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTCATTGCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTTCATTTTAGAAGTAACCACTCTTGT
 CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG
 CCGATTGCTTGAGGTCAAGTGTTTGGACAGCCTGGCCAACATGGCGAAACCCCATCTACT
 AAAAAATACAAAAATTAGCCAGGCATGGTGGTGGTGCCTGTAATCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTGAACCCGGGGGCGAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
 TGCACCTAGCCTGGGGAGAAAAGTAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA
 AAAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCC
 AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAAATTCCTCTAATATGACTTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTTELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGGCCGCAACACTCCGTCTCACCCCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCCAAGGTGTT
 GGTACAGCTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCCCTTACCTGGACAG
GATGAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTATTATTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGTGGCTGGCA
 GCCTCGCCCAACGAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC
 AGCCAACTACTTTGCGTTTAAAACTGTCAGTGGGGCCGCCAACGTCGTGGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC
 GCCCTGGTGAATGGAACACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCCTGGTGTGCTGGTG
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTG
 GGGAGTTCTACGCAAAACAACTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAAGCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGC
 TGTGGCTCTTCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCTTGCACGC
 TGTGTCGCGCCTCTCCTCCTCGAAACAGAACCCTCCACAGCACATCTACCCGGAAGACC
 AGCCTCAGAGGGTCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGTCTTTCGTGAGG
 ACTGCTGACGGCTGGTCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA
 TTTTTGCTGGTTTTGAAAAAAAAAAAAAAAAAAAA

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLRLLALIFAIVTTWTFIRSYSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRLFSDLGSSYAKQLGFRDSWVFIGA
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCTCTGGGGAT
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCTGGAAGCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTTAGTCTCTAGTCTCAAATCCCAGTCCC
 CTGCAACCCCTTCTGGGACACTATGTGTCTCCGCCCTCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTTGGCCA
 GCCTCTTACCCTGAGTGTGGAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT
 GACATTTGACCCTGATTGCTGTCTGCAGCCCCACGGATATGACCAGCCTGGCACCCGAGC
 CTTTGGACCTGCACAACAATGGCCACACAGTGCACCTCTCTCTGCCCTCTACCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC
 CCCAGGGGGTCAAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCCTGGCT
 GTCTGGGCATCCTAATTGAGGTGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACCTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG
 AGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCAGATTTCAATGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
 CCTTCTCCTGGCTGTTTATTTCATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTCACCTCAGCACAGCCACGACTGAGGCATTAAATTCCTTCTCAGATACCA
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCCTGGACATCTCTTAGAGAG
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAATCTGTTTAGTTGCAGGG
 GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATA
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGTATCAATA
 TATTGGAAATTAAAGTTTCTGACTTT

FIGURE 242

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTI
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCICLLLVAVYF
IARKIRKKRLNKRKSVVFTSAQATTEA
```

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTC
 GTGGACCCAAAGGTAGCAATCTGAAAC**ATG**AGGAGTACGATTCTACTGTTTTGTCTTCTAGG
 ATCAACTCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACGGCTC
 CGGATCAGGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTG
 ATACCATTAAACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG
 AATGACACCTGGTACCAGACCCACCCATTGACCCTGGGAGGGTGAATGTACAACAGCAAC
 TGCACCCACATGTGTTACCAATTTTGTACACAACCTGGAGCCAGGGCACATCCTAAGC
 TCAGAGGAATTGCCACAAATCTTCAGAGCCTCATCATCCATTCTTGTTCCCGGGAGGCAT
 CCTGCCCACCAGTCAGGCAGGGGCTAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAG
 GAGCAGGTGTAATCTTGCCACCCAGGGAACCCAGCAGGCCGCTCCCAACTCCCAGTGGC
 ACAGATGACGACTTTGCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA
 GGAAGCCACCACAGAATCAGCAAATGGAATTCAG**TAA**GCTGTTTCAAATTTTTCAACTAAG
 CTGCCTCGAATTTGGTGATACATGTGAATCTTTATCATTGATTATATTATGGAATAGATTGA
 GACACATTGGATAGTCTTAGAAGAAATTAATTCCTTAATTTACCTGAAAATATTCTTGAAAT
 TCAGAAAATATGTTCTATGTAGAGAAATCCCAACTTTTAAAAACAATAATCAATGGATAAAT
 CTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTAACATATTGAAAA
 ACTGAA
 AAAAAAAAAAAAAAAAAAAAA

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPAIGLPPTKLPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSIPAGGAGVNPATQCTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 245

GGAGAGAGGCGCGGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCCTCGGAGCGCGGCG
 GAGCCAGACGCTGACCACGTTCCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCG
 GCAGCCGGGAGCCCATGCGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCTCC
 TGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCTTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCGGGTACACCTG
 GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAG
 GAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
 TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCTCAGCGTTGGTATTTACATTC
 AATGGAGCTGAATGTTTCAAGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAG
 CCCTGAAATGAATCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
 GAATTGGTGTGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAA
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAAGTACCCAAATA
AATGCTTTAATTTTCATTTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACCTTAAAT
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
 CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT
 GGTTCATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
 TAATTTGGAATATTGTTGTGGTCTTTTGTCTTCTTAGTATAGCATTTTTTAAAAAATA
 TAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAAT
 AAAAATTATTTCCAACA

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
PGRDGSPGANVPGTPGIPGRDGFKEGECLEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIVLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

249/249-249